



RECEIVED
DEC 02 2003
TECH CENTER 1600/2900

SEQUENCE LISTING

<110> FOX, GARY M.
JING, SHUQIAN
WEN, DUANZHI

<120> GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR

<130> A-401D

<140> 08/866,354
<141> 1997-05-30

<150> US 60/015,907
<151> 1996-04-22

<150> US 60/017,221
<151> 1996-05-09

<150> US 08/837,199
<151> 1997-04-14

<160> 61

<170> PatentIn version 3.2

<210> 1
<211> 2568
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (540)..(1934)

<220>
<221> misc_feature
<222> (2078)..(2078)
<223> N in position 2078 indicates a position of divergence between
different receptor clones

<220>
<221> misc_feature
<222> (2107)..(2107)
<223> N in position 2107 indicates a position of divergence between
different receptor clones

<220>
<221> misc_feature
<222> (2241)..(2241)
<223> N in position 2241 indicates a position of divergence between
different receptor clones

<220>
<221> misc_feature
<222> (2250)..(2250)
<223> N in position 2250 indicates a position of divergence between
different receptor clones

<220>
<221> misc_feature
<222> (2256)..(2294)
<223> N in positions 2256 to 2294 indicates positions of divergence

between different receptor clones

```

<400> 1
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa      60
cgagcatccg agccgagggc tctgctcgga aatcgctctg gcccaactcg gcccttcgag      120
ctctcgaaga ttaccgcac tatttttttt ttcttttttt tcttttctta gcgcagataa      180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag      240
taaataaaca aactggctcc tcgccgcagc tggacgcggg cggttgagtc caggttgggt      300
cggacctgaa cccctaaaag cggaaccgcc tccgcacctc gccatcccg agctgagtcg      360
ccggcggcgg tggtgctgc cagaccggga gtttctcttt tcaactggatg gagctgaact      420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa      480
gaccagcgg cggtcggga tttttttggg ggggcgggga ccagccccgc gccggcacc      539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc      587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc      635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg      683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc      731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60
ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag      779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80
cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag      827
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95
aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga      875
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110
aat gat ctg ctg gag gat tcc cca tat gaa cca gtt aac agc aga ttg      923
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125
tca gat ata ttc cgg gtg gtc cca ttc ata tca gat gtt ttt cag caa      971
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140
gtg gag cac att ccc aaa ggg aac aac tgc ctg gat gca gcg aag gcc      1019
Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160
tgc aac ctc gac gac att tgc aag aag tac agg tcg gcg tac atc acc      1067
Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

```

cgc	tgc	acc	acc	agc	gtg	tcc	aac	gat	gtc	tgc	aac	cgc	cgc	aag	tgc	1115
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
cac	aag	gcc	ctc	cgg	cag	ttc	ttt	gac	aag	gtc	cgc	gcc	aag	cac	agc	1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
		195					200					205				
tac	gga	atg	ctc	ttc	tgc	tcc	tgc	cgg	gac	atc	gcc	tgc	aca	gag	cgg	1211
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
	210					215					220					
agg	cga	cag	acc	atc	gtg	cct	gtg	tgc	tcc	tat	gaa	gag	agg	gag	aag	1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	
225					230					235					240	
ccc	aac	tgt	ttg	aat	ttg	cag	gac	tcc	tgc	aag	acg	aat	tac	atc	tgc	1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
				245					250					255		
aga	tct	cgc	ctt	gcg	gat	ttt	ttt	acc	aac	tgc	cag	cca	gag	tca	agg	1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
			260					265					270			
tct	gtc	agc	agc	tgt	cta	aag	gaa	aac	tac	gct	gac	tgc	ctc	ctc	gcc	1403
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
			275				280					285				
tac	tcg	ggg	ctt	att	ggc	aca	gtc	atg	acc	ccc	aac	tac	ata	gac	tcc	1451
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
agt	agc	ctc	agt	gtg	gcc	cca	tgg	tgt	gac	tgc	agc	aac	agt	ggg	aac	1499
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
gac	cta	gaa	gag	tgc	ttg	aaa	ttt	ttg	aat	ttc	ttc	aag	gac	aat	aca	1547
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325				330						335		
tgt	ctt	aaa	aat	gca	att	caa	gcc	ttt	ggc	aat	ggc	tcc	gat	gtg	acc	1595
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
gtg	tgg	cag	cca	gcc	ttc	cca	gta	cag	acc	acc	act	gcc	act	acc	acc	1643
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
		355					360					365				
act	gcc	ctc	cgg	gtt	aag	aac	aag	ccc	ctg	ggg	cca	gca	ggg	tct	gag	1691
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
aat	gaa	att	ccc	act	cat	gtt	ttg	cca	ccg	tgt	gca	aat	tta	cag	gca	1739
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	
cag	aag	ctg	aaa	tcc	aat	gtg	tcg	ggc	aat	aca	cac	ctc	tgt	att	tcc	1787
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Asn	Thr	His	Leu	Cys	Ile	Ser	
				405					410					415		
aat	ggt	aat	tat	gaa	aaa	gaa	ggt	ctc	ggt	gct	tcc	agc	cac	ata	acc	1835
Asn	Gly	Asn	Tyr	Glu	Lys	Glu	Gly	Leu	Gly	Ala	Ser	Ser	His	Ile	Thr	
			420					425					430			

aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg 1883
 Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
 435 440 445

gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa aca 1931
 Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
 450 455 460

tca tagctgcatt aaaaaaatac aatatggaca tgtaaaaaga caaaaaccaa 1984
 Ser
 465

gttatctggtt tctgtttctc ttgtatagct gaaattccag tttaggagct cagttgagaa 2044

acagttccat tcaactggaa cattttttttt tttncctttt aagaaagctt cttgtgatcc 2104

ttnggggctt ctgtgaaaaa cctgatgcag tgctccatcc aaactcagaa ggctttggga 2164

tatgctgtat tttaaaggga cagtttgtaa cttgggctgt aaagcaaact ggggctgtgt 2224

tttcgatgat gatgatnatc atgatnatga tnnnnnnnnnn nnnnnnnnnnn nnnnnnnnnnn 2284

nnnnnnnnnn gattttaaca gttttacttc tggcctttcc tagctagaga aggagttaat 2344

atttctaagg taactcccat atctccttta atgacattga tttctaataga tataaatttc 2404

agcctacatt gatgccaagc ttttttgcca caaagaagat tcttaccaag agtgggcttt 2464

gtggaaacag ctggtactga tgttcacctt tatatatgta ctagcatttt ccacgctgat 2524

gtttatgtac tgtaaacagt tctgcactct tgtacaaaag aaaa 2568

<210> 2
 <211> 465
 <212> PRT
 <213> HUMAN

<400> 2

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
450 455 460

Ser
465

<210> 3
<211> 2138
<212> DNA
<213> RAT

<220>
<221> CDS
<222> (302)..(1705)

<400> 3
agctcgctct cccggggcag tgggtgtggat gcaccggagt tcgggcgctg ggcaagttgg 60
gtcgggaactg aaccctgaa agcgggtccg cctcccgccc tcgcgcccgc ccggatctga 120
gtcgtctggcg gcggtgggcg gcagagcgac ggggagtctg ctctcaccct ggatggagct 180
gaactttgag tggccagagg agcgcagtcg cccggggatc gctgcacgct gagctctctc 240
cccagaccg ggcggcggct ttggattttg gggggggcggg gaccagctgc gcggcggcac 300
c atg ttc cta gcc act ctg tac ttc gcg ctg cca ctc ctg gat ttg ctg 349
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
atg tcc gcc gag gtg agt ggt gga gac cgt ctg gac tgt gtg aaa gcc 397
Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

agc Ser	gat Asp	cag Gln 35	tgc Cys	ctg Leu	aag Lys	gaa Glu 40	cag Gln	agc Ser	tgc Cys	agc Ser	acc Thr	aag Lys 45	tac Tyr	cgc Arg	aca Thr	445
cta Leu	agg Arg 50	cag Gln	tgc Cys	gtg Val	gcg Ala	ggc Gly 55	aag Lys	gaa Glu	acc Thr	aac Asn	ttc Phe 60	agc Ser	ctg Leu	aca Thr	tcc Ser	493
ggc Gly 65	ctt Leu	gag Glu	gcc Ala	aag Lys	gat Asp 70	gag Glu	tgc Cys	cgt Arg	agc Ser	gcc Ala 75	atg Met	gag Glu	gcc Ala	ttg Leu	aag Lys 80	541
cag Gln	aag Lys	tct Ser	ctg Leu	tac Tyr 85	aac Asn	tgc Cys	cgc Arg	tgc Cys	aag Lys 90	cgg Arg	ggc Gly	atg Met	aag Lys	aaa Lys 95	gag Glu	589
aag Lys	aat Asn	tgt Cys	ctg Leu 100	cgt Arg	atc Ile	tac Tyr	tgg Trp	agc Ser 105	atg Met	tac Tyr	cag Gln	agc Ser	ctg Leu 110	cag Gln	gga Gly	637
aat Asn	gac Asp	ctc Leu 115	ctg Leu	gaa Glu	gat Asp	tcc Ser	ccg Pro 120	tat Tyr	gag Glu	ccg Pro	gtt Val	aac Asn 125	agc Ser	agg Arg	ttg Leu	685
tca Ser	gat Asp	ata Ile 130	ttc Phe	cgg Arg	gca Ala	gtc Val 135	ccg Pro	ttc Phe	ata Ile	tca Ser	gat Asp 140	gtt Val	ttc Phe	cag Gln	caa Gln	733
gtg Val 145	gaa Glu	cac His	att Ile	tcc Ser	aaa Lys 150	ggg Gly	aac Asn	aac Asn	tgc Cys	ctg Leu 155	gac Asp	gca Ala	gcc Ala	aag Lys	gcc Ala 160	781
tgc Cys	aac Asn	ctg Leu	gac Asp	gac Asp	acc Thr	tgt Cys	aag Lys	aag Lys	tac Tyr 170	agg Arg	tcg Ser	gcc Ala	tac Tyr	atc Ile 175	acc Thr	829
ccc Pro	tgc Cys	acc Thr	acc Thr	agc Ser	atg Met	tcc Ser	aac Asn	gag Glu 185	gtc Val	tgc Cys	aac Asn	cgc Arg	cgt Arg	aag Lys	tgc Cys	877
cac His	aag Lys	gcc Ala 195	ctc Leu	agg Arg	cag Gln	ttc Phe	ttc Phe 200	gac Asp	aag Lys	gtt Val	ccg Pro	gcc Ala 205	aag Lys	cac His	agc Ser	925
tac Tyr	ggg Gly 210	atg Met	ctc Leu	ttc Phe	tgc Cys	tcc Ser 215	tgc Cys	cgg Arg	gac Asp	atc Ile	gcc Ala 220	tgc Cys	acc Thr	gag Glu	cgg Arg	973
cgg Arg 225	cga Arg	cag Gln	act Thr	atc Ile	gtc Val 230	ccc Pro	gtg Val	tgc Cys	tcc Ser	tat Tyr 235	gaa Glu	gaa Glu	cga Arg	gag Glu	agg Arg 240	1021
ccc Pro	aac Asn	tgc Cys	ctg Leu	agt Ser 245	ctg Leu	caa Gln	gac Asp	tcc Ser	tgc Cys 250	aag Lys	acc Thr	aat Asn	tac Tyr	atc Ile 255	tgc Cys	1069
aga Arg	tct Ser	cgc Arg	ctt Leu 260	gca Ala	gat Asp	ttt Phe	ttt Phe 265	acc Thr	aac Asn	tgc Cys	cag Gln	cca Pro	gag Glu	tca Ser	agg Arg	1117
tct Ser	gtc Val	agc Ser 275	aac Asn	tgt Cys	ctt Leu	aag Lys	gag Glu 280	aac Asn	tac Tyr	gca Ala	gac Asp	tgc Cys 285	ctc Leu	ctg Leu	gcc Ala	1165

tac	tcg	gga	ctg	att	ggc	aca	gtc	atg	act	ccc	aac	tac	gta	gac	tcc	1213
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	
	290					295					300					
agc	agc	ctc	agc	gtg	gca	cca	tgg	tgt	gac	tgc	agc	aac	agc	ggc	aat	1261
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
gac	ctg	gaa	gac	tgc	ttg	aaa	ttt	ctg	aat	ttt	ttt	aag	gac	aat	act	1309
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
tgt	ctc	aaa	aat	gca	att	caa	gcc	ttt	ggc	aat	ggc	tca	gat	gtg	acc	1357
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
atg	tgg	cag	cca	gcc	cct	cca	gtc	cag	acc	acc	act	gcc	acc	act	acc	1405
Met	Trp	Gln	Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
		355					360					365				
act	gcc	ttc	cgg	gtc	aag	aac	aag	cct	ctg	ggg	cca	gca	ggg	tct	gag	1453
Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
aat	gag	atc	ccc	aca	cac	gtt	tta	cca	ccc	tgt	gcg	aat	ttg	cag	gct	1501
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	
cag	aag	ctg	aaa	tcc	aat	gtg	tcg	ggg	agc	aca	cac	ctc	tgt	ctt	tct	1549
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	Ser	
				405					410					415		
gat	agt	gat	ttc	gga	aag	gat	ggg	ctc	gct	ggg	gcc	tcc	agc	cac	ata	1597
Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	Ile	
			420					425					430			
acc	aca	aaa	tca	atg	gct	gct	cct	ccc	agc	tgc	agt	ctg	agc	tca	ctg	1645
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu	
		435					440					445				
ccg	gtg	ctg	atg	ctc	acc	gcc	ctt	gct	gcc	ctg	tta	tct	gta	tcg	ttg	1693
Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Ala	Leu	Leu	Ser	Val	Ser	Leu	
	450					455					460					
gca	gaa	acg	tcg	tagctgcac	cgaggaaaaca	gtatgaaaag	acaaaagaga									1745
Ala	Glu	Thr	Ser													
465																
accaagtatt	ctgtccctgt	cctcttgtat	atctgaaaat	ccagttttta	aagctccggt											1805
gagaagcagt	ttcacccaac	tggaactcct	tccttgtttt	taagaaagct	tgtggccctc											1865
aggggcttct	gttgaagaac	tgctacaggg	ctaattccaa	accataagg	ctctggggcg											1925
tggtgcggct	taaggggacc	atttgcacca	tgtaaagcaa	gctgggctta	tcatgtgttt											1985
gatggtgagg	atggtagtgg	tgatgatgat	ggtaatttta	acagcttgaa	ccctgttctc											2045
tctactgggt	aggaacagga	gatactattg	ataaagattc	ttccatgtct	tactcagcag											2105
cattgccttc	tgaagacagg	cccgacagccg	tcg													2138

<211> 468

<212> PRT

<213> RAT

<400> 4

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
225 230 235 240

Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
405 410 415

Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
420 425 430

Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu
435 440 445

Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
450 455 460

Ala Glu Thr Ser
465

<210> 5
<211> 3209

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(510)
<223> note="1 to 510 is -237 to 272 of Fig 5 Hsgr-21bf"

<220>
<221> misc_feature
<222> (1)..(539)
<223> note="1 to 539 is -237 to 301 of Fig 5 Gdnfr"

<220>
<221> CDS
<222> (540)..(1937)

<220>
<221> misc_feature
<222> (1091)..(1091)
<223> N in position 1091 indicates any nucleic acid

<220>
<221> misc_feature
<222> (2078)..(2078)
<223> N in position 2078 indicates a position of divergence between different receptor clones

<220>
<221> misc_feature
<222> (2256)..(2294)
<223> N in positions 2256 to 2294 indicates positions of divergence between different receptor clones

```

<400> 5
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa      60
cgagcatccg agccgagggc tctgctcgga aatcgctctg gcccaactcg gcccttcgag      120
ctctcgaaga ttaccgcac tatttttttt ttcttttttt tcttttccta gcgcagataa      180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag      240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt      300
cggacctgaa cccctaaaag cggaaccgcc tcccgccctc gccatcccgg agctgagtcg      360
ccggcgggcg tggctgctgc cagaccggga gtttctctct tcaactggatg gagctgaact      420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa      480
gaccagcgcg cggtctggga tttttttggg ggggcgggga ccagccccgc gccggcacc      539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc      587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1          5          10          15

ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc      635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20          25          30

```

agt Ser	gat Asp	cag Gln 35	tgc Cys	ctg Leu	aag Lys	gag Glu 40	cag Gln	agc Ser	tgc Cys	agc Ser	acc Thr 45	aag Lys	tac Tyr	cgc Arg	acg Thr	683
cta Leu	agg Arg 50	cag Gln	tgc Cys	gtg Val	gcg Ala	ggc Gly 55	aag Lys	gag Glu	acc Thr	aac Asn	ttc Phe 60	agc Ser	ctg Leu	gca Ala	tcc Ser	731
ggc Gly 65	ctg Leu	gag Glu	gcc Ala	aag Lys	gat Asp 70	gag Glu	tgc Cys	cgc Arg	agc Ser	gcc Ala 75	atg Met	gag Glu	gcc Ala	ctg Leu	aag Lys 80	779
cag Gln	aag Lys	tcg Ser	ctc Leu	tac Tyr 85	aac Asn	tgc Cys	cgc Arg	tgc Cys	aag Lys 90	cgg Arg	ggg Gly	atg Met	aag Lys 95	aag Lys	gag Glu	827
aag Lys	aac Asn	tgc Cys	ctg Leu 100	cgc Arg	att Ile	tac Tyr	tgg Trp	agc Ser 105	atg Met	tac Tyr	cag Gln	agc Ser	ctg Leu 110	cag Gln	gga Gly	875
aat Asn	gat Asp	ctg Leu 115	ctg Leu	gag Glu	gat Asp	tcc Ser	cca Pro 120	tat Tyr	gaa Glu	cca Pro	gtt Val 125	aac Asn	agc Ser	aga Arg	ttg Leu	923
tca Ser	gat Asp	ata Ile 130	ttc Phe	cgg Arg	gtg Val	gtc Val 135	cca Pro	ttc Phe	ata Ile	tca Ser	gat Asp 140	gtt Val	ttt Phe	cag Gln	caa Gln	971
gtg Val 145	gag Glu	cac His	att Ile	ccc Pro	aaa Lys 150	ggg Gly	aac Asn	aac Asn	tgc Cys	ctg Leu 155	gat Asp	gca Ala	gcg Ala	aag Lys	gcc Ala 160	1019
tgc Cys	aac Asn	ctc Leu	gac Asp	gac Asp	att Ile	tgc Cys	aag Lys	aag Lys	tac Tyr 170	agg Arg	tcg Ser	gcg Ala	tac Tyr	atc Ile 175	acc Thr	1067
ccg Pro	tgc Cys	acc Thr 180	acc Thr	agc Ser	gtg Val	tcc Ser	aan Xaa	gat Asp 185	gtc Val	tgc Cys	aac Asn	cgc Arg	cgc Arg	aag Lys	tgc Cys	1115
cac His	aag Lys	gcc Ala 195	ctc Leu	cgg Arg	cag Gln	ttc Phe	ttt Phe 200	gac Asp	aag Lys	gtc Val	ccg Pro	gcc Ala 205	aag Lys	cac His	agc Ser	1163
tac Tyr	gga Gly 210	atg Met	ctc Leu	ttc Phe	tgc Cys	tcc Ser	tgc Cys	cgg Arg	gac Asp	atc Ile	gcc Ala 220	tgc Cys	aca Thr	gag Glu	cgg Arg	1211
agg Arg 225	cga Arg	cag Gln	acc Thr	atc Ile	gtg Val 230	cct Pro	gtg Val	tgc Cys	tcc Ser	tat Tyr 235	gaa Glu	gag Glu	agg Arg	gag Glu	aag Lys 240	1259
ccc Pro	aac Asn	tgt Cys	ttg Leu	aat Asn 245	ttg Leu	cag Gln	gac Asp	tcc Ser	tgc Cys 250	aag Lys	acg Thr	aat Asn	tac Tyr 255	atc Ile	tgc Cys	1307
aga Arg	tct Ser	cgc Arg	ctt Leu 260	gcg Ala	gat Asp	ttt Phe	ttt Phe 265	acc Thr	aac Asn	tgc Cys	cag Gln	cca Pro	gag Glu 270	tca Ser	agg Arg	1355
tct Ser	gtc Val	agc Ser 275	agc Ser	tgt Cys	cta Leu	aag Lys	gaa Glu 280	aac Asn	tac Tyr	gct Ala	gac Asp	tgc Cys 285	ctc Leu	ctc Leu	gcc Ala	1403

[illegible]

```

gaaacagctg gtactgatgt tcacctttat atatgtacta gcattttcca cgctgatgtt 2527
tatgtactgt aaacagttct gcaactcttg acaaaagaaa aaacacctgt cacatccaaa 2587
tatagtatct gtcttttcgt caaaatagag agtggggaat gagtgtgccg attcaatacc 2647
tcaatccctg aacgacactc tctaatacct aagccttacc tgagtgagaa gccctttacc 2707
taacaaaagt ccaatatagc tgaaatgtcg ctctaatact ctttacacat atgaggttat 2767
atgtagaaaa aaattttact actaaatgat ttcaactatt ggctttctat attttgaaag 2827
taatgatatt gtctcatttt tttactgatg gtttaataca aaatacacag agcttggttc 2887
ccctcataag tagtgttcgc tctgatatga acttcacaaa tacagctcat caaaagcaga 2947
ctctgagaag cctcgtgctg tagcagaaaag ttctgcatca tgtgactgtg gacaggcagg 3007
agggaaacaga acagacaagc attgtctttt gtcattgctc gaagtgaag cgtgcatacc 3067
tgtggaggga actggtggct gcttgtaa atgtctgcagc atctcttgac acacttgtea 3127
tgacacaatc cagtaccttg gttttcaggt tatctgacaa aggcagcttt gattgggaca 3187
tggaggcatg ggcaggccgg aa 3209

```

```

<210> 6
<211> 465
<212> PRT
<213> HUMAN

<220>
<221> misc_feature
<222> (184)..(184)
<223> The 'Xaa' at location 184 stands for Lys, or Asn.

<400> 6

```

```

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1          5          10          15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20          25          30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35          40          45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50          55          60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65          70          75          80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85          90          95

```

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Val Ser Xaa Asp Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
 225 230 235 240
 Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
 290 295 300
 Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
 305 310 315 320
 Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
 325 330 335
 Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
 340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr
450 455 460

Ser
465

<210> 7
<211> 508
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(508)
<223> Note="1 to 508 is -235 to 272 of Figure 5 Hsgr-21af"

<400> 7
tctggcctcg gaacacgcca ttctccgcgc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggctc tgctcggaaa tcgtcctggc ccaactcggc ctttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataaacaaa ctggctcctc gccgcagctg gacgcggctg gttgagtcca gggtgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccggag ctgagtcgcc 360
ggcggcggtg gctgctgcca gaccgggagt ttctctttt actggatgga gctgaacttt 420
gggcggccag agcagcacag ctgtccgggg atcgctgcac gctgagctcc ctcggaaga 480
cccagcggcg gctcgggatt tttttggg 508

<210> 8

<211> 510
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(510)
<223> Note="1 to 510 is -237 to 272 of Figure 5 Hsgr-21bf"

<400> 8
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tttttttttt ttcttttttt tcttttccta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttggggt 300
cggacctgaa cccctaaaag cggaaccgcc tcccgcctc gccatcccgg agctgagtcg 360
ccggcggcgg tggctgctgc cagaccggga gtttcctctt tcaactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccacgcgg cggctcggga tttttttggg 510

<210> 9
<211> 1927
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(537)
<223> Note= "1 to 537 is -235 to 301 of Figure 5 21acon"

<220>
<221> CDS
<222> (538)..(1926)

<220>
<221> misc_feature
<222> (550)..(550)
<223> N in position 550 indicates any nucleic acid

<400> 9
tctggcctcg gaacacgcca ttctccgcgc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggctc tgctcgga aa tcgtcctggc ccaactcggc ctttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccggga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataa caaaa ctggctcctc gccgcagctg gacgcggctg gttgagtcca ggttgggctc 300
gacctgaacc cctaaaagcg gaaccgcctc ccgcctcgc catcccggag ctgagtcgcc 360
ggcggcgggtg gctgctgcca gaccggagt ttctctttt actggatgga gctgaacttt 420

gggcggccag agcagcacag ctgtccgggg atcgctgcac gctgagctcc ctcggcaaga	480
cccagcggcg gctcgggatt tttttggggg ggcggggacc agccccgcgc cggcacc	537
atg ttc ctg gcg ncc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu 1 5 10 15	585
ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala 20 25 30	633
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr 35 40 45	681
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser 50 55 60	729
ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys 65 70 75 80	777
cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag Gln Lys Ser Leu Tyr 85 Asn Cys Arg Cys Lys 90 Arg Gly Met Lys 95 Lys Glu	825
aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly 100 105 110	873
aat gat ctg ctg gag gat tcc cca tat gaa cca gtt aac agc aga ttg Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu 115 120 125	921
tca gat ata ttc cgg gtg gtc cca ttc ata tca gat gtt ttt cag caa Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln 130 135 140	969
gtg gag cac att ccc aaa ggg aac aac tgc ctg gat gca gcg aag gcc Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala 145 150 155 160	1017
tgc aac ctc gac gac att tgc aag aag tac agg tcg gcg tac atc acc Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr 165 170 175	1065
ccg tgc acc acc agc gtg tcc aac gat gtc tgc aac cgc cgc aag tgc Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys 180 185 190	1113
cac aag gcc ctc cgg cag ttc ttt gac aag gtc ccg gcc aag cac agc His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser 195 200 205	1161
tac gga atg ctc ttc tgc tcc tgc cgg gac atc gcc tgc aca gag cgg Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg 210 215 220	1209
agg cga cag acc atc gtg cct gtg tgc tcc tat gaa gag agg gag aag Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys 225 230 235 240	1257

ccc aac tgt ttg aat ttg cag gac tcc tgc aag acg aat tac atc tgc	1305
Pro Asn Cys Leu Asn 245 Leu Gln Asp Ser Cys 250 Lys Thr Asn Tyr Ile Cys 255	
aga tct cgc ctt gcg gat ttt ttt acc aac tgc cag cca gag tca agg	1353
Arg Ser Arg Leu 260 Ala Asp Phe Phe Thr 265 Asn Cys Gln Pro Glu 270 Ser Arg	
tct gtc agc agc tgt cta aag gaa aac tac gct gac tgc ctc ctc gcc	1401
Ser Val Ser Ser Cys Leu Lys Glu 280 Asn Tyr Ala Asp Cys 285 Leu Leu Ala	
tac tcg ggg ctt att ggc aca gtc atg acc ccc aac tac ata gac tcc	1449
Tyr Ser Gly Leu Ile Gly Thr 295 Val Met Thr Pro Asn Tyr Ile Asp Ser	
agt agc ctc agt gtg gcc cca tgg tgt gac tgc agc aac agt ggg aac	1497
Ser Ser Leu Ser Val 310 Ala Pro Trp Cys Asp Cys 315 Ser Asn Ser Gly Asn 320	
gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca	1545
Asp Leu Glu Glu Cys 325 Leu Lys Phe Leu Asn 330 Phe Phe Lys Asp Asn Thr 335	
tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc gat gtg acc	1593
Cys Leu Lys Asn 340 Ala Ile Gln Ala Phe 345 Gly Asn Gly Ser Asp 350 Val Thr	
gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc act acc acc	1641
Val Trp Gln Pro Ala Phe Pro Val 360 Gln Thr Thr Thr Ala Thr Thr Thr 365	
act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca ggg tct gag	1689
Thr Ala Leu Arg Val Lys 375 Asn Lys Pro Leu Gly Pro 380 Ala Gly Ser Glu	
aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat tta cag gca	1737
Asn Glu Ile Pro Thr 390 His Val Leu Pro Pro Cys 395 Ala Asn Leu Gln Ala 400	
cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc	1785
Gln Lys Leu Lys 405 Ser Asn Val Ser Gly Asn 410 Thr His Leu Cys Ile Ser 415	
aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc	1833
Asn Gly Asn Tyr 420 Glu Lys Glu Gly Leu 425 Gly Ala Ser Ser His Ile Thr	
aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg	1881
Thr Lys Ser Met Ala Ala Pro 440 Ser Cys Gly Leu Ser Pro Leu Leu 445	
gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa a	1927
Val Leu Val Val Thr Ala 455 Ser Thr Leu Leu Ser Leu Thr Glu 460	

<210> 10
 <211> 463
 <212> PRT
 <213> HUMAN

<220>

<221> misc_feature

<222> (5)..(5)

<223> The 'Xaa' at location 5 stands for Thr, Ala, Pro, or Ser.

<400> 10

Met Phe Leu Ala Xaa Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 11
<211> 1929
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(539)
<223> Note= "1 to 539 is -237 to 301 of Figure 5 21bcon"

<220>
<221> CDS
<222> (540)..(1928)

<400> 11
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcggg aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tattttttttt ttctttttttt tcttttctcta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcg ggacaccatt gccctgaaag aataaataag 240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt 300
cggacctgaa cccctaaaag cggaaccgcc tccgccttc gccatcccgg agctgagtcg 360
ccggcggcgg tggctgctgc cagaccggga gtttctctt tcaactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccagcgg cggtcggga tttttttggg ggggcgggga ccagccccgc gccggcacc 539
atg ttc ctg gcg acc ctg tac ttc gcg ctg ccg ctc ttg gac ttg ctc 587
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15
ctg tcg gcc gaa gtg agc ggc gga gac cgc ctg gat tgc gtg aaa gcc 635
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30
agt gat cag tgc ctg aag gag cag agc tgc agc acc aag tac cgc acg 683
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45
cta agg cag tgc gtg gcg ggc aag gag acc aac ttc agc ctg gca tcc 731
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60
ggc ctg gag gcc aag gat gag tgc cgc agc gcc atg gag gcc ctg aag 779
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80
cag aag tcg ctc tac aac tgc cgc tgc aag cgg ggt atg aag aag gag 827
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95
aag aac tgc ctg cgc att tac tgg agc atg tac cag agc ctg cag gga 875
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110
aat gat ctg ctg gag gat tcc cca tat gaa cca gtt aac agc aga ttg 923
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125
tca gat ata ttc cgg gtg gtc cca ttc ata tca gat gtt ttt cag caa 971
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

gtg	gag	cac	att	ccc	aaa	ggg	aac	aac	tgc	ctg	gat	gca	gcg	aag	gcc	1019
Val	Glu	His	Ile	Pro	Lys	Gly	Asn	Asn	Cys	Leu	Asp	Ala	Ala	Lys	Ala	
145					150					155					160	
tgc	aac	ctc	gac	gac	att	tgc	aag	aag	tac	agg	tcg	gcg	tac	atc	acc	1067
Cys	Asn	Leu	Asp	Asp	Ile	Cys	Lys	Lys	Tyr	Arg	Ser	Ala	Tyr	Ile	Thr	
				165					170					175		
ccg	tgc	acc	acc	agc	gtg	tcc	aac	gat	gtc	tgc	aac	cgc	cgc	aag	tgc	1115
Pro	Cys	Thr	Thr	Ser	Val	Ser	Asn	Asp	Val	Cys	Asn	Arg	Arg	Lys	Cys	
			180					185					190			
cac	aag	gcc	ctc	cgg	cag	ttc	ttt	gac	aag	gtc	ccg	gcc	aag	cac	agc	1163
His	Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Ala	Lys	His	Ser	
		195					200					205				
tac	gga	atg	ctc	ttc	tgc	tcc	tgc	cgg	gac	atc	gcc	tgc	aca	gag	cgg	1211
Tyr	Gly	Met	Leu	Phe	Cys	Ser	Cys	Arg	Asp	Ile	Ala	Cys	Thr	Glu	Arg	
	210					215					220					
agg	cga	cag	acc	atc	gtg	cct	gtg	tgc	tcc	tat	gaa	gag	agg	gag	aag	1259
Arg	Arg	Gln	Thr	Ile	Val	Pro	Val	Cys	Ser	Tyr	Glu	Glu	Arg	Glu	Lys	
225					230					235					240	
ccc	aac	tgt	ttg	aat	ttg	cag	gac	tcc	tgc	aag	acg	aat	tac	atc	tgc	1307
Pro	Asn	Cys	Leu	Asn	Leu	Gln	Asp	Ser	Cys	Lys	Thr	Asn	Tyr	Ile	Cys	
				245				250						255		
aga	tct	cg	ctt	gcg	gat	ttt	ttt	acc	aac	tgc	cag	cca	gag	tca	agg	1355
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg	
			260					265					270			
tct	gtc	agc	agc	tgt	cta	aag	gaa	aac	tac	gct	gac	tgc	ctc	ctc	gcc	1403
Ser	Val	Ser	Ser	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala	
			275				280					285				
tac	tcg	ggg	ctt	att	ggc	aca	gtc	atg	acc	ccc	aac	tac	ata	gac	tcc	1451
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Ile	Asp	Ser	
	290					295					300					
agt	agc	ctc	agt	gtg	gcc	cca	tgg	tgt	gac	tgc	agc	aac	agt	ggg	aac	1499
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn	
305					310					315					320	
gac	cta	gaa	gag	tgc	ttg	aaa	ttt	ttg	aat	ttc	ttc	aag	gac	aat	aca	1547
Asp	Leu	Glu	Glu	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr	
				325					330					335		
tgt	ctt	aaa	aat	gca	att	caa	gcc	ttt	ggc	aat	ggc	tcc	gat	gtg	acc	1595
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr	
			340					345					350			
gtg	tgg	cag	cca	gcc	ttc	cca	gta	cag	acc	acc	act	gcc	act	acc	acc	1643
Val	Trp	Gln	Pro	Ala	Phe	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr	
			355				360					365				
act	gcc	ctc	cgg	gtt	aag	aac	aag	ccc	ctg	ggg	cca	gca	ggg	tct	gag	1691
Thr	Ala	Leu	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu	
	370					375					380					
aat	gaa	att	ccc	act	cat	gtt	ttg	cca	ccg	tgt	gca	aat	tta	cag	gca	1739
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala	
385					390					395					400	

cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc 1787
Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc 1835
Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg 1883
Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca gaa a 1929
Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 12
<211> 463
<212> PRT
<213> HUMAN

<400> 12

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Pro Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser
405 410 415

Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr
420 425 430

Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu
435 440 445

Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
450 455 460

<210> 13
<211> 699
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(699)
<223> Note= "1 to 699 is 814 to 1512 of Figure 5 Hsgr-29a"

<220>
<221> CDS
<222> (2)..(697)

<400> 13
g tcg gcg tac atc acc ccg tgc acc acc agc gtg tcc aat gat gtc tgc 49
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

aac cgc cgc aag tgc cac aag gcc ctc cgg cag ttc ttt gac aag gtc 97
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

ccg gcc aag cac agc tac gga atg ctc ttc tgc tcc tgc cgg gac atc 145
Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

gcc tgc aca gag cgg agg cga cag acc atc gtg cct gtg tgc tcc tat 193
Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
50 55 60

gaa gag agg gag aag ccc aac tgt ttg aat ttg cag gac tcc tgc aag 241
Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65 70 75 80

acg aat tac atc tgc aga tct cgc ctt gcg gat ttt ttt acc aac tgc 289
Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
85 90 95

cag cca gag tca agg tct gtc agc agc tgt cta aag gaa aac tac gct 337
Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100 105 110

gac tgc ctc ctc gcc tac tcg ggg ctt att ggc aca gtc atg acc ccc 385
Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115 120 125

aac tac ata gac tcc agt agc ctc agt gtg gcc cca tgg tgt gac tgc 433
Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

```

agc aac agt ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc      481
Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145                               150                               155                               160

ttc aag gac aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat      529
Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
                               165                               170                               175

ggc tcc gat gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc      577
Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
                               180                               185                               190

act gcc gct acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg      625
Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
                               195                               200                               205

cca gca ggg tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt      673
Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
                               210                               215                               220

gca aat tta cag gca cag aag ctg aa      699
Ala Asn Leu Gln Ala Gln Lys Leu
225                               230

<210> 14
<211> 232
<212> PRT
<213> HUMAN

<400> 14

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1                               5                               10                               15

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
                               20                               25                               30

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
                               35                               40                               45

Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
                               50                               55                               60

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65                               70                               75                               80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
                               85                               90                               95

Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
                               100                               105                               110

Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
                               115                               120                               125

```

Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145 150 155 160

Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165 170 175

Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180 185 190

Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195 200 205

Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210 215 220

Ala Asn Leu Gln Ala Gln Lys Leu
225 230

<210> 15
<211> 2157
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(2157)
<223> Note= "1 to 2157 is 814 to 2971 of Figure 5 29brc"

<220>
<221> CDS
<222> (2)..(886)

<220>
<221> misc_feature
<222> (1204)..(1242)
<223> N in positions 1204 to 1242 indicates positions of divergence
between different receptor clones.

<400> 15
g tcg gcg tac atc acc ccg tgc acc acc agc gtg tcc aat gat gtc tgc 49
Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1 5 10 15

aac cgc cgc aag tgc cac aag gcc ctc ccg cag ttc ttt gac aag gtc 97
Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20 25 30

ccg gcc aag cac agc tac gga atg ctc ttc tgc tcc tgc cgg gac atc 145
Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35 40 45

gcc tgc aca gag cgg agg cga cag acc atc gtg cct gtg tgc tcc tat	193
Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr	
50 55 60	
gaa gag agg gag aag ccc aac tgt ttg aat ttg cag gac tcc tgc aag	241
Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys	
65 70 75 80	
acg aat tac atc tgc aga tct cgc ctt gcg gat ttt ttt acc aac tgc	289
Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys	
85 90 95	
cag cca gag tca agg tct gtc agc agc tgt cta aag gaa aac tac gct	337
Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala	
100 105 110	
gac tgc ctc ctc gcc tac tcg ggg ctt att ggc aca gtc atg acc ccc	385
Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro	
115 120 125	
aac tac ata gac tcc agt agc ctc agt gtg gcc cca tgg tgt gac tgc	433
Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys	
130 135 140	
agc aac agt ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc	481
Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe	
145 150 155 160	
ttc aag gac aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat	529
Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn	
165 170 175	
ggc tcc gat gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc	577
Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr	
180 185 190	
act gcc gct acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg	625
Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly	
195 200 205	
cca gca ggg tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt	673
Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys	
210 215 220	
gca aat tta cag gca cag aag ctg aaa tcc aat gtg tcg ggc aat aca	721
Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr	
225 230 235 240	
cac ctc tgt att tcc aat ggt aat tat gaa aaa gaa ggt ctc ggt gct	769
His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala	
245 250 255	
tcc agc cac ata acc aca aaa tca atg gct gct cct cca agc tgt ggt	817
Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly	
260 265 270	
ctg agc cca ctg ctg gtc ctg gtg gta acc gct ctg tcc acc cta tta	865
Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu	
275 280 285	
tct tta aca gaa aca tca tag ctgcattaaa aaaatacaat atggacatgt	916
Ser Leu Thr Glu Thr Ser	
290	

```

aaaaagacaa aaaccaagtt atctgtttcc tgttctcttg tatagctgaa attccagttt 976
aggagctcag ttgagaaaca gttccattca actggaacat tttttttttt ccttttaaga 1036
aagcttcttg tgatccttcg gggcttctgt gaaaaacctg atgcagtgtc ccatccaaac 1096
tcagaaggct ttgggatatg ctgtatttta aaggacagct ttgtaacttg ggctgtaaag 1156
caaactgggg ctgtgttttc gatgatgatg atcatcatga tcatgatnnn nnnnnnnnnn 1216
nnnnnnnnnn nnnnnnnnnn nnnnnngatt ttaacagttt tacttctggc ctttcctagc 1276
tagagaagga gttaatatct ctaaggtaac tcccatatct cttttaatga cattgatttc 1336
taatgatata aatttcagcc tacattgatg ccaagctttt ttgccacaaa gaagattctt 1396
accaagagtg ggctttgttg aaacagctgg tactgatgtt cacctttata tatgtactag 1456
cattttccac gctgatgttt atgtactgta aacagttctg cactcttgta caaaagaaaa 1516
aacacctgtc acatccaaat atagtatctg tcttttcgtc aaaatagaga gtggggaatg 1576
agtgtgccga ttcaatacct caatccctga acgacactct cctaataccta agccttacct 1636
gagtgagaag ccctttacct aacaaaagtc caatatagct gaaatgtcgc tctaatactc 1696
tttacacata tgaggttata tgtagaaaaa aattttacta ctaaagtatt tcaactattg 1756
gctttctata ttttgaaagt aatgatattg tctcattttt ttactgatgg tttaatacaa 1816
aatacacaga gcttgtttcc cctcataagt agtggtcgtc ctgatatgaa cttcacaaat 1876
acagctcatc aaaagcagac tctgagaagc ctggtgctgt agcagaaagt tctgcatcat 1936
gtgactgtgg acaggcagga ggaaacagaa cagacaagca ttgtcttttg tcattgctcg 1996
aagtgcaagc gtgcatacct gtggagggaa ctggtggctg cttgtaaattg ttctgcagca 2056
tctcttgaca cacttgatcat gacacaatcc agtaccttg ttttcagggt atctgacaaa 2116
ggcagctttg attgggacat ggaggcatgg gcaggccgga a 2157

```

```

<210> 16
<211> 294
<212> PRT
<213> HUMAN

```

```

<400> 16

```

```

Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser Asn Asp Val Cys
1          5          10          15

```

```

Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
20          25          30

```

```

Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
35          40          45

```

```

Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
50          55          60

```

Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys
65 70 75 80

Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
85 90 95

Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala
100 105 110

Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
115 120 125

Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
130 135 140

Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe
145 150 155 160

Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
165 170 175

Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr
180 185 190

Thr Ala Ala Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly
195 200 205

Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
210 215 220

Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr
225 230 235 240

His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala
245 250 255

Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly
260 265 270

Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu
275 280 285

Ser Leu Thr Glu Thr Ser
290

<210> 17
<211> 659

<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(659)
<223> Note= "1 to 659 is 1033 to 1691 of Figure 5 Hsgr-21ar"

<220>
<221> CDS
<222> (2)..(658)

<400> 17

g aat ttg cag gac tcc tgc aag acg aat tac atc tgc aga tct cgc ctt	49
Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu	
1 5 10 15	
gcg gat ttt ttt acc aac tgc cag cca gag tca agg tct gtc agc agc	97
Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser	
20 25 30	
tgt cta aag gaa aac tac gct gac tgc ctc ctc gcc tac tcg ggg ctt	145
Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu	
35 40 45	
att ggc aca gtc atg acc ccc aac tac ata gac tcc agt agc ctc agt	193
Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser	
50 55 60	
gtg gcc cca tgg tgt gac tgc agc aac agt ggg aac gac cta gaa gag	241
Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu	
65 70 75 80	
tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca tgt ctt aaa aat	289
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn	
85 90 95	
gca att caa gcc ttt ggc aat ggc tcc gat gtg acc gtg tgg cag cca	337
Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro	
100 105 110	
gcc ttc cca gta cag acc acc act gcc act acc acc act gcc ctc cgg	385
Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg	
115 120 125	
gtt aag aac aag ccc ctg ggg cca gca ggg tct gag aat gaa att ccc	433
Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro	
130 135 140	
act cat gtt ttg cca ccg tgt gca aat tta cag gca cag aag ctg aaa	481
Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys	
145 150 155 160	
tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc aat ggt aat tat	529
Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr	
165 170 175	
gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc aca aaa tca atg	577
Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met	
180 185 190	

gct gct cct cca agc tgt ggt ctg agc cca ctg ctg gtc ctg gtg gta 625
Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
195 200 205

acc gct ctg tcc acc cta tta tct tta aca gaa a 659
Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
210 215

<210> 18
<211> 219
<212> PRT
<213> HUMAN

<400> 18

Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu
1 5 10 15

Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser
20 25 30

Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu
35 40 45

Ile Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser
50 55 60

Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu
65 70 75 80

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
85 90 95

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
100 105 110

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
115 120 125

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
130 135 140

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
145 150 155 160

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
165 170 175

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
180 185 190

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
195 200 205

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu
210 215

<210> 19
<211> 630
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(630)
<223> Note= "1 to 630 is 1062 to 1691 of Figure 5 Hsgr-21br"

<220>
<221> CDS
<222> (3)..(629)

<400> 19
ac atc tgc aga tct cgc ctt gcg gat ttt ttt acc aac tgc cag cca 47
Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro
1 5 10 15
gag tca agg tct gtc agc agc tgt cta aag gaa aac tac gct gac tgc 95
Glu Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys
20 25 30
ctc ctc gcc tac tcg ggg ctt att ggc aca gtc atg acc ccc aac tac 143
Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr
35 40 45
ata gac tcc agt agc ctc agt gtg gcc cca tgg tgt gac tgc agc aac 191
Ile Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn
50 55 60
agt ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag 239
Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys
65 70 75
gac aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc 287
Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser
80 85 90 95
gat gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc 335
Asp Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala
100 105 110
act acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca 383
Thr Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala
115 120 125
ggg tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat 431
Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn
130 135 140
tta cag gca cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc 479
Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu
145 150 155

tgt att tcc aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc 527
Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser 175
160 165 170

cac ata acc aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc 575
His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser 190
180 185

cca ctg ctg gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta 623
Pro Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu 205
195 200

aca gaa a 630
Thr Glu

<210> 20
<211> 209
<212> PRT
<213> HUMAN

<400> 20

Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu
1 5 10 15

Ser Arg Ser Val Ser Ser Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu
20 25 30

Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Ile
35 40 45

Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser
50 55 60

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
65 70 75 80

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
85 90 95

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
100 105 110

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
115 120 125

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
130 135 140

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
145 150 155 160

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
165 170 175

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
180 185 190

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
195 200 205

Glu

<210> 21
<211> 1075
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1075)
<223> Note= "1 to 1075 is 1255 to 2330 of Figure 5 Hsgr-2"

<220>
<221> CDS
<222> (2)..(445)

<220>
<221> misc_feature
<222> (763)..(801)
<223> N in position 763 to 801 indicates positions of divergence
between different receptor clones.

<400> 21
t ggg aac gac cta gaa gag tgc ttg aaa ttt ttg aat ttc ttc aag gac 49
Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
1 5 10 15
aat aca tgt ctt aaa aat gca att caa gcc ttt ggc aat ggc tcc gat 97
Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
20 25 30
gtg acc gtg tgg cag cca gcc ttc cca gta cag acc acc act gcc act 145
Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
35 40 45
acc acc act gcc ctc cgg gtt aag aac aag ccc ctg ggg cca gca ggg 193
Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
50 55 60
tct gag aat gaa att ccc act cat gtt ttg cca ccg tgt gca aat tta 241
Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
65 70 75 80
cag gca cag aag ctg aaa tcc aat gtg tcg ggc aat aca cac ctc tgt 289
Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
85 90 95

```

att tcc aat ggt aat tat gaa aaa gaa ggt ctc ggt gct tcc agc cac      337
Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
                  100                      105                      110

ata acc aca aaa tca atg gct gct cct cca agc tgt ggt ctg agc cca      385
Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
                  115                      120                      125

ctg ctg gtc ctg gtg gta acc gct ctg tcc acc cta tta tct tta aca      433
Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
                  130                      135                      140

gaa aca tca tag ctgcattaaa aaaatacaat atggacatgt aaaaagacaa      485
Glu Thr Ser
145

aaaccaagtt atctgtttcc tgttctcttg tatagctgaa attccagttt aggagctcag      545
ttgagaaaca gttccattca actggaacat tttttttttt ccttttaaga aagcttcttg      605
tgatccttcg gggcttctgt gaaaaacctg atgcagtgtc ccatccaaac tcagaaggct      665
ttgggatatg ctgtatttta aaggagacagt ttgtaacttg ggctgtaaag caaactgggg      725
ctgtgttttc gatgatgatg atcatcatga tcatgatnnn nnnnnnnnnn nnnnnnnnnn      785
nnnnnnnnnn nnnnnngatt ttaacagttt tacttctggc ctttcctagc tagagaagga      845
gttaatatatt ctaaggtaac tcccatatct cttttaatga cattgatttc taatgatata      905
aatttcagcc tacattgatg ccaagctttt ttgccacaaa gaagattctt accaagagtg      965
ggctttgtgg aaacagctgg tactgatgtt cacctttata tatgtactag cattttccac      1025
gctgatgttt atgtactgta aacagttctg cactcttgta caaaagaaaa      1075

```

<210> 22
 <211> 147
 <212> PRT
 <213> HUMAN

<400> 22

```

Gly Asn Asp Leu Glu Glu Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp
1          5          10          15

Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp
          20          25          30

Val Thr Val Trp Gln Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr
          35          40          45

Thr Thr Thr Ala Leu Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly
          50          55          60

Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu
65          70          75          80

```

Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys
85 90 95

Ile Ser Asn Gly Asn Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His
100 105 110

Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro
115 120 125

Leu Leu Val Leu Val Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr
130 135 140

Glu Thr Ser
145

<210> 23
<211> 1059
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1059)
<223> Note= "1 to 1059 is 1272 to 2330 of Figure 5 Hsgr-9"

<220>
<221> CDS
<222> (3)..(428)

<400> 23
ag tgc ttg aaa ttt ttg aat ttc ttc aag gac aat aca tgt ctt aaa 47
Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys
1 5 10 15

aat gca att caa gcc ttt ggc aat ggc tcc gat gtg acc gtg tgg cag 95
Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln
20 25 30

cca gcc ttc cca gta cag acc acc act gcc act acc acc act gcc ctc 143
Pro Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu
35 40 45

cgg gtt aag aac aag ccc ctg ggg cca gca ggg tct gag aat gaa att 191
Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile
50 55 60

ccc act cat gtt ttg cca ccg tgt gca aat tta cag gca cag aag ctg 239
Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu
65 70 75

aaa tcc aat gtg tcg ggc aat aca cac ctc tgt att tcc aat ggt aat 287
Lys Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn
80 85 90 95

tat gaa aaa gaa ggt ctc ggt gct tcc agc cac ata acc aca aaa tca 335
Tyr Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser
100 105 110

```

atg gct gct cct cca agc tgt ggt ctg agc cca ctg ctg gtc ctg gtg      383
Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val
              115                      120                      125

gta acc gct ctg tcc acc cta tta tct tta aca gaa aca tca tag      428
Val Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
              130                      135                      140

ctgcattaaa aaaatacaat atggacatgt aaaaagacaa aaaccaagtt atctgtttcc      488

tggttctcttg tatagctgaa attccagttt aggagctcag ttgagaaaca gttccattca      548

actggaacat tttttttttt tccttttaag aaagcttctt gtgatccttt ggggcttctg      608

tgaaaaacct gatgcagtgc tccatccaaa ctgagaaggc tttgggatat gctgtatttt      668

aaagggacag tttgtaactt gggctgtaaa gcaaactggg gctgtgtttt cgatgatgat      728

gatgatcatg atgatgatca tcatgatcat gatgatgatc atcatgatca tgatgatgat      788

tttaacagtt ttacttctgg cttttcctag ctagagaagg agttaatatt tctaaggtaa      848

ctcccatatc tcctttaatg acattgattt ctaatgatat aaatttcagc ctacattgat      908

gccaagcttt tttgccacaa agaagattct taccaagagt gggctttgtg gaaacagctg      968

gtactgatgt tcacctttat atatgtacta gcattttcca cgctgatgtt tatgtactgt    1028

aaacagttct gcactcttgt acaaaagaaa a                                1059

```

```

<210> 24
<211> 141
<212> PRT
<213> HUMAN

```

<400> 24

```

Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn
1              5              10              15

Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro
              20              25              30

Ala Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg
              35              40              45

Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro
50              55              60

Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys
65              70              75              80

Ser Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr
              85              90              95

Glu Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met
100              105              110

```

Ala Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val
115 120 125

Thr Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
130 135 140

<210> 25
<211> 10
<212> PRT
<213> HUMAN

<400> 25

Gln Ser Cys Ser Thr Lys Tyr Arg Thr Leu
1 5 10

<210> 26
<211> 10
<212> PRT
<213> HUMAN

<400> 26

Cys Lys Arg Gly Met Lys Lys Glu Lys Asn
1 5 10

<210> 27
<211> 10
<212> PRT
<213> HUMAN

<400> 27

Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val
1 5 10

<210> 28
<211> 10
<212> PRT
<213> RAT

<400> 28

Cys Ser Tyr Glu Glu Arg Glu Arg Pro Asn
1 5 10

<210> 29
<211> 14
<212> PRT
<213> RAT

<400> 29

Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr
1 5 10

<210> 30
<211> 21
<212> DNA
<213> HUMAN

<400> 30
ctgtttgaat ttgcaggact c 21

<210> 31
<211> 36
<212> DNA
<213> HUMAN

<400> 31
ctcctctcta agcttctaac cacagcttgg aggagc 36

<210> 32
<211> 37
<212> DNA
<213> HUMAN

<400> 32
ctcctctcta agcttctatg ggctcagacc acagctt 37

<210> 33
<211> 60
<212> DNA
<213> HUMAN

<400> 33
ctcctctcta agcttctact tgtcatcgtc gtccttgtag tcaccacagc ttggaggagc 60

<210> 34
<211> 60
<212> DNA
<213> HUMAN

<400> 34
ctcctctcta agcttctact tgtcatcgtc gtccttgtag tctggctcag accacagctt 60

<210> 35
<211> 4232
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (1587)..(2978)

<400> 35
catgaagaaa cctcagtaag tctcagactt ggcccaaagg agcccaacta gttactccct 60
gggtctgttac agaggatctg gctattacac tcaacagcaa aaattcaatt caatcccgt 120
aaagatataa gaatcactag gaakaataag ccagaactca agacagaaat agcattaagt 180
agttccttca gtacagtgag cagaagctgg ccactctacg actctawaag actcagaaaa 240

gcttactagg gaccwctggg catwccggtg tcctatgtgg ggatttcgta acgtctttga	300
gtcagaagct gccctcaaaa tagtttcttc tcaaaacggg ttcaggcttt gttagaaagg	360
gaagacttca ctgccacttt acccagatca tctaccccat ccttggaatg aatggggaag	420
cttcagccac cctaccaggc tcctaaaatc accaacttga gagaaaaact ataacgttgc	480
tctaccagta cttcaggagg ttaaagaaag tcacagaaga aaagaactct ggggaaaaca	540
gtcaaattcg gctattaaga cattagttac agggccctgt acctctctc tagaaaccct	600
gggagtacac ccgcagagga gagagagccc aagccaccaa gcaaagtcaa ccaatctggc	660
aaaggggctg cccactgcgg ctttcagtc aagaagtgga tcctgctggg tcgcagtcct	720
tcttctatct cctcacttcc tatttaccct ttgaagtggg tactgaatag cccgttccca	780
agcagaggcc ctttgtatac ggggtgctac agtcgcctgg tggaaacacc ttggcagagt	840
tgtttggtgc caggatgggc cactgaaggc atctgctgtg gacacacaca cacacacaca	900
cacacacaca cacacacaca gagagaggag agagaaagac acacgcacgc agagacacac	960
ggtcactgga attccattag aaaaaagtga gccgagcaag ggtagcggg agaagatttt	1020
tttgaatctt gtcttcgtct tgggtgcgaa gaagcgactc cagtctctcg tcctcgaagc	1080
tccgactgga ttgttcttgg gcgctgacac ccgtctgtgg atttcttttc tatttgcat	1140
ttattccgac cccctccctc gccgcttct tccagccctt cactcgcaaa tcgcctctct	1200
ccccacctcc ccaggccct cctgggaagc gcaggggaat tggaccgcg gggactcacg	1260
ccttcccga cgattggagg ggagggctga cccaggact gggctgttgg cttagaaagc	1320
cgatacacag atacgcgtat atttgattgt agcgggcaag gggggcgtcg agaggcagca	1380
gcccacgccc cgctctcac cccacccct ccagccagag gcgagaatcg caggactcgg	1440
gatcttcac ggggtggacta gctgggatct ccgcattgga tttggggctg attaccactg	1500
cttggctatt attattgttg ttgttactac tattatTTTT ttttacccaa gggagaaaga	1560
caaaaaaacg gtgggattta tttaac atg atc ttg gca aac gtc ttc tgc ctc	1613
Met Ile Leu Ala Asn Val Phe Cys Leu	
1 5	
ttc ttc ttt cta gac gac acc ctc cgc tct ttg gcc agc cct tcc tcc	1661
Phe Phe Phe Leu Asp Asp Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser	
10 15 20 25	
ctg cag ggc ccc gag ctc cac ggc tgg cgc ccc cca gtg gac tgt gtc	1709
Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val	
30 35 40	
cgg gcc aat gag ctg tgt gcc gcc gaa tcc aac tgc agc tct cgc tac	1757
Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Arg Tyr	
45 50 55	
cgc act ctg cgg cag tgc ctg gca ggc cgc gac cgc aac acc atg ctg	1805
Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu	
60 65 70	

gcc	aac	aag	gag	tgc	cag	gcg	gcc	ttg	gag	gtc	ttg	cag	gag	agc	ccg	1853
Ala	Asn	Lys	Glu	Cys	Gln	Ala	Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	
75						80					85					
ctg	tac	gac	tgc	cgc	tgc	aag	cgg	ggc	atg	aag	aag	gag	ctg	cag	tgt	1901
Leu	Tyr	Asp	Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	
90					95					100					105	
ctg	cag	atc	tac	tgg	agc	atc	cac	ctg	ggg	ctg	acc	gag	ggt	gag	gag	1949
Leu	Gln	Ile	Tyr	Trp	Ser	Ile	His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	
				110					115					120		
ttc	tac	gaa	gcc	tcc	ccc	tat	gag	ccg	gtg	acc	tcc	cgc	ctc	tcg	gac	1997
Phe	Tyr	Glu	Ala	Ser	Pro	Tyr	Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	
			125					130					135			
atc	ttc	agg	ctt	gct	tca	atc	ttc	tca	ggg	aca	ggg	gca	gac	ccg	gtg	2045
Ile	Phe	Arg	Leu	Ala	Ser	Ile	Phe	Ser	Gly	Thr	Gly	Ala	Asp	Pro	Val	
		140					145					150				
gtc	agc	gcc	aag	agc	aac	cat	tgc	ctg	gat	gct	gcc	aag	gcc	tgc	aac	2093
Val	Ser	Ala	Lys	Ser	Asn	His	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	
155						160					165					
ctg	aat	gac	aac	tgc	aag	aag	ctg	cgc	tcc	tcc	tac	atc	tcc	atc	tgc	2141
Leu	Asn	Asp	Asn	Cys	Lys	Lys	Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	
170					175					180					185	
aac	cgc	gag	atc	tcg	ccc	acc	gag	cgc	tgc	aac	cgc	cgc	aag	tgc	cac	2189
Asn	Arg	Glu	Ile	Ser	Pro	Thr	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	
				190					195					200		
aag	gcc	ctg	cgc	cag	ttc	ttc	gac	cgg	gtg	ccc	agc	gag	tac	acc	tac	2237
Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	
			205				210						215			
cgc	atg	ctc	ttc	tgc	tcc	tgc	caa	gac	cag	gcg	tgc	gct	gag	cgc	cgc	2285
Arg	Met	Leu	Phe	Cys	Ser	Cys	Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	
		220					225					230				
cgg	caa	acc	atc	ctg	ccc	agc	tgc	tcc	tat	gag	gac	aag	gag	aag	ccc	2333
Arg	Gln	Thr	Ile	Leu	Pro	Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	
235						240					245					
aac	tgc	ctg	gac	ctg	cgt	ggc	gtg	tgc	cgg	act	gac	cac	ctg	tgt	cgg	2381
Asn	Cys	Leu	Asp	Leu	Arg	Gly	Val	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	
250					255					260					265	
tcc	cgg	ctg	gcc	gac	ttc	cat	gcc	aat	tgt	cga	gcc	tcc	tac	cag	acg	2429
Ser	Arg	Leu	Ala	Asp	Phe	His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Gln	Thr	
				270					275					280		
gtc	acc	agc	tgc	cct	gcg	gac	aat	tac	cag	gcg	tgt	ctg	ggc	tct	tat	2477
Val	Thr	Ser	Cys	Pro	Ala	Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	
			285					290					295			
gct	ggc	atg	att	ggg	ttt	gac	atg	aca	cct	aac	tat	gtg	gac	tcc	agc	2525
Ala	Gly	Met	Ile	Gly	Phe	Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Ser	
		300					305					310				
ccc	act	ggc	atc	gtg	gtg	tcc	ccc	tgg	tgc	agc	tgt	cgt	ggc	agc	ggg	2573
Pro	Thr	Gly	Ile	Val	Val	Ser	Pro	Trp	Cys	Ser	Cys	Arg	Gly	Ser	Gly	
		315				320					325					

aac atg gag gag gag tgt gag aag ttc ctc agg gac ttc acc gag aac Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn 330 335 340 345	2621
cca tgc ctc cgg aac gcc atc cag gcc ttt ggc aac ggc acg aac gtg Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asn Val 350 355 360	2669
aac gtg tcc cca aaa ggc ccc tcg ttc cag gcc acc cag gcc cct cgg Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg 365 370 375	2717
gtg gag aag acg cct tct ttg cca gat gac ctc agt gac agt acc agc Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser 380 385 390	2765
ttg ggg acc agt gtc atc acc acc tgc acg tct gtc cag gag cag ggg Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly 395 400 405	2813
ctg aag gcc aac aac tcc aaa gag tta agc atg tgc ttc aca gag ctc Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu 410 415 420 425	2861
acg aca aat atc atc cca ggg agt aac aag gtg atc aaa cct aac tca Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser 430 435 440	2909
ggc ccc agc aga gcc aga ccg tcg gct gcc ttg acc gtg ctg tct gtc Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val 445 450 455	2957
ctg atg ctg aaa ctg gcc ttg taggctgtgg gaaccgagtc agaagatttt Leu Met Leu Lys Leu Ala Leu 460	3008
tgaaagctac gcagacaaga acagccgcct gacgaaatgg aaacacacac agacacacac	3068
acaccttgca aaaaaaaaaat tgtttttccc accttgctgc tgaacctgtc tcctcccagg	3128
tttcttctct ggagaagttt ttgtaaacca aacagacaag caggcaggca gcctgagagc	3188
tggcccaggg gtcccctggc aggggaaact ctggtgccgg ggagggcacg aggtctctaga	3248
aatgcccttc actttctcct ggtgtttttc tctctggacc cttctgaagc agagaccgga	3308
caagagcctg cagcgggaagg gactctgggc tgtgcctgag gctggctggg ggcaggacaa	3368
cacagctgct tccccaggct gccactctg gggaccgcgt gggggctggc agagggcatc	3428
ggtcagcggg gcagcggggc tggccatgag ggtccacctt cagccctttg gcttcaagga	3488
tggagatggg tttgccctcc ctctctgccc tcgggtgggg ctggtgggtc tgcagctggg	3548
gtgggaactt ccccacggat ggcggtggag ggggttcgca ccgtgctggg ctccccctga	3608
ctgtagcacg gagtggtggg gctggggggc agctccagga gggcttgaga gctcagcctg	3668
cctgggagag cccttggtggc gaggcattaa aacttgggca ccagcttctt tctcgtgggc	3728
agaaattttg aagtcagaga gaaacggtcc tttgttggtc tctttgcttt ctcgtgggtc	3788
ctttggcagg cctccctttg gggagaggga ggggagagac cacagccggg tgtgtgtctg	3848

cagcaccgtg ggccctcaag ctttctgct gtcttctccc tctctctctt ttcccttttc 3908
tcttttctca tttcctagac gtacgtcaac tgtatgtaca taccgggggt cctctcctaa 3968
catatatgta tatacacatc catatacata tattgtgtgg tttccctttt ctttcctttt 4028
tttaagcaac aaaactatgg aaataatacc ccaacagatg agcgaaaatg tattattgta 4088
aagtttattt tttttaatac tggtgtctat aatggggaaa aaggacattg gccccgcagt 4148
gccctgcccc agtcagcctg gctgggctct ggtggggggt cctgatccgc atccaagctt 4208
aaccaaggct ccaataaacg tgcg 4232

<210> 36
<211> 464
<212> PRT
<213> HUMAN

<400> 36

Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Asp Thr
1 5 10 15

Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
20 25 30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
35 40 45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
50 55 60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65 70 75 80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
100 105 110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
115 120 125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
130 135 140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145 150 155 160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
165 170 175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
180 185 190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
195 200 205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
210 215 220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
225 230 235 240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
245 250 255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
260 265 270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
275 280 285

Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
290 295 300

Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser
305 310 315 320

Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
325 330 335

Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
340 345 350

Gln Ala Phe Gly Asn Gly Thr Asn Val Asn Val Ser Pro Lys Gly Pro
355 360 365

Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
370 375 380

Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
385 390 395 400

Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
405 410 415

Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
420 425 430

Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro
435 440 445

Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu
450 455 460

<210> 37
<211> 1991
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (203)..(1402)

<400> 37
caagtcaaag gtttaatcat gatccaagag cccagagaga ctttaggaca ataataggaa 60
taaagcaagg cccacaggct ccagctcctg atgccagat gttcggcagg atccggggac 120
agggcagtgcc aggcagtagt tttccatcct ccattccaggg gaggagcgcg gggagcgcgg 180
agcccgggcgc ctacagctcg cc atg gtg cgc ccc ctg aac ccg cga ccg ctg 232
Met Val Arg Pro Leu Asn Pro Arg Pro Leu
1 5 10
ccg ccc gta gtc ctg atg ttg ctg ctg ctg ctg ccg ccg tcg ccg ctg 280
Pro Pro Val Val Leu Met Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu
15 20 25
cct ctc gca gcc gga gac ccc ctt ccc aca gaa agc cga ctc atg aac 328
Pro Leu Ala Ala Gly Asp Pro Leu Pro Thr Glu Ser Arg Leu Met Asn
30 35 40
agc tgt ctc cag gcc agg agg aag tgc cag gct gat ccc acc tgc agt 376
Ser Cys Leu Gln Ala Arg Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser
45 50 55
gct gcc tac cac cac ctg gat tcc tgc acc tct agc ata agc acc cca 424
Ala Ala Tyr His His Leu Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro
60 65 70
ctg ccc tca gag gag cct tcg gtc cct gct gac tgc ctg gag gca gca 472
Leu Pro Ser Glu Glu Pro Ser Val Pro Ala Asp Cys Leu Glu Ala Ala
75 80 85 90
cag caa ctc agg aac agc tct ctg ata ggc tgc atg tgc cac cgg cgc 520
Gln Gln Leu Arg Asn Ser Ser Leu Ile Gly Cys Met Cys His Arg Arg
95 100 105
atg aag aac cag gtt gcc tgc ttg gac atc tat tgg acc gtt cac cgt 568
Met Lys Asn Gln Val Ala Cys Leu Asp Ile Tyr Trp Thr Val His Arg
110 115 120
gcc cgc agc ctt ggt aac tat gag ctg gat gtc tcc ccc tat gaa gac 616
Ala Arg Ser Leu Gly Asn Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp
125 130 135

aca	gtg	acc	agc	aaa	ccc	tgg	aaa	atg	aat	ctc	agc	aaa	ctg	aac	atg	664
Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	
	140					145					150					
ctc	aaa	cca	gac	tca	gac	ctc	tgc	ctc	aag	ttt	gcc	atg	ctg	tgt	act	712
Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	
	155				160					165					170	
ctc	aat	gac	aag	tgt	gac	cgg	ctg	cgc	aag	gcc	tac	ggg	gag	gcg	tgc	760
Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	
				175					180					185		
tcc	ggg	ccc	cac	tgc	cag	cgc	cac	gtc	tgc	ctc	agg	cag	ctg	ctc	act	808
Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	
			190					195					200			
ttc	ttc	gag	aag	gcc	gcc	gag	ccc	cac	gcg	cag	ggc	ctg	cta	ctg	tgc	856
Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	
		205					210					215				
cca	tgt	gcc	ccc	aac	gac	cgg	ggc	tgc	ggg	gag	cgc	cgg	cgc	aac	acc	904
Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	
	220					225					230					
atc	gcc	ccc	aac	tgc	gcg	ctg	ccg	cct	gtg	gcc	ccc	aac	tgc	ctg	gag	952
Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	
	235				240				245						250	
ctg	cgg	cgc	ctc	tgc	ttc	tcc	gac	ccg	ctt	tgc	aga	tca	cgc	ctg	gtg	1000
Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	
				255					260					265		
gat	ttc	cag	acc	cac	tgc	cat	ccc	atg	gac	atc	cta	gga	act	tgt	gca	1048
Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	
			270					275					280			
aca	gag	cag	tcc	aga	tgt	cta	cga	gca	tac	ctg	ggg	ctg	att	ggg	act	1096
Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	
		285					290					295				
gcc	atg	acc	ccc	aac	ttt	gcc	agc	aat	gtc	aac	acc	agt	gtt	gcc	tta	1144
Ala	Met	Thr	Pro	Asn	Phe	Ala	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	
	300					305					310					
agc	tgc	acc	tgc	cga	ggc	agt	ggc	aac	ctg	cag	gag	gag	tgt	gaa	atg	1192
Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	
	315				320					325					330	
ctg	gaa	ggg	ttc	ttc	tcc	cac	aac	ccc	tgc	ctc	acg	gag	gcc	att	gca	1240
Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	
				335					340					345		
gct	aag	atg	cgt	ttt	cac	agc	caa	ctc	ttc	tcc	cag	gac	tgg	cca	cac	1288
Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	
			350					355					360			
cct	acc	ttt	gct	gtg	atg	gca	cac	cag	aat	gaa	aac	cct	gct	gtg	agg	1336
Pro	Thr	Phe	Ala	Val	Met	Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	
		365				370						375				
cca	cag	ccc	tgg	gtg	ccc	tct	ctt	ttc	tcc	tgc	acg	ctt	ccc	ttg	att	1384
Pro	Gln	Pro	Trp	Val	Pro	Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	
	380					385					390					

ctg ctc ctg agc cta tgg tagctggact tccccagggc cctcttcccc 1432
 Leu Leu Leu Ser Leu Trp
 395 400

tccaccacac ccaggtggac ttgcagccca caaggggtga ggaaaggaca gcagcaggaa 1492
 ggaggtgcag tgcgcagatg agggcacagg agaagctaag ggttatgacc tccagatcct 1552
 tactggtcca gtcctcattc cctccacccc atctccactt ctgattcatg ctgccccctcc 1612
 ttggtggcca caatttagcc atgtcatctg gtggtgacca gctccaccaa gcccccttgt 1672
 gagcccttcc tcttgactac caggatcacc agaataaat aagttagcct ttctctattg 1732
 cattccagat taggggttagg gtagggagga ctgggtgttc tgaggcagcc tagaaagtca 1792
 ttctcctttg tgaagaaggc tcctgcccc tcgtctctc ctctgagtgg aggatggaaa 1852
 actactgcct gcaactgcct gtccccggat cctgccgaac atctgggcat caggagctgg 1912
 agcctgtggg ccttgcttta ttcctattat tgtcctaaag tctctctggg ctcttggatc 1972
 atgattaaac ctttgactg 1991

<210> 38
 <211> 400
 <212> PRT
 <213> HUMAN

<400> 38

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
 1 5 10 15

Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30

Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45

Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60

Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80

Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95

Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
 100 105 110

Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
 115 120 125

Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140

Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160

Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175

Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190

Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205

Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220

Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240

Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255

Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270

His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285

Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300

Ala Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320

Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335

His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350

Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365

Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380

Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
385 390 395 400

<210> 39
<211> 2215
<212> DNA
<213> RAT

<220>
<221> CDS
<222> (684)..(2063)

<400> 39
gcgggccgcgt cgaccttgac catgcagaca ctttttcagg cctctgtctg gtgtgaagtt 60
ggcagataca agcaaggccc gaaaggggtc tcagcttctc tctcctgggc ctcttgact 120
gagttaggct tgcttctggt tgtcttctaa aggcacgggtg atacagaatg atgagactag 180
gctggagggg gctttctgct tctctgtgtg tgaccttgag ttatctccct tcgttgatc 240
cgagctttcc tggaatatga tgttgaatat gaatatgagt tctgcctaag gtccagacag 300
gctctgaggg ttaactgact tttggagcct tcaaataaat accttggatg gagtgggggt 360
ttgtccaatg ggagttgagg caagatccct ttgcataagc cttgccacat catgttgaag 420
ccatgccatt ctgtctggac tattggcatc ttacctttcc agcagtttca gtgaaggcct 480
tcctggatth atcattctgt gttccactgc ctaggattgt gctcaagagg aaatgaatgt 540
gaaccatggt ttagggggag tatggccaac cagggttgggt ctgtgttgac cttggtcttg 600
gtgttctttt gtgtaaagtg ggtgagaagt tccttcaaac cttaggccta cattgggggtc 660
agagactgtg gtggccctca ttc atg ctt gtc ttc cct tcc cac tac cca gac 713
Met Leu Val Phe Pro Ser His Tyr Pro Asp
1 5 10
gaa acc ctc cgc tct ttg gcc agc cct tcc tcc ctg cag ggc tct gag 761
Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu
15 20 25
ctc cac ggc tgg cgc ccc caa gtg gac tgt gtc cgg gcc aat gag ctg 809
Leu His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu
30 35 40
tgt gcg gct gaa tcc aac tgc agc tcc agg tac cgc acc ctt cgg cag 857
Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln
45 50 55
tgc ctg gca ggc cgg gat cgc aat acc atg ctg gcc aat aag gag tgc 905
Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys
60 65 70
cag gca gcc ctg gag gtc ttg cag gaa agc cca ctg tat gac tgc cgc 953
Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg
75 80 85 90

tgc	aag	cgg	ggc	atg	aag	aag	gag	ctg	cag	tgt	ctg	cag	atc	tac	tgg	1001
Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	
			95						100					105		
agc	atc	cat	ctg	ggg	ctg	aca	gag	ggg	gag	gag	ttc	tat	gaa	gct	tcc	1049
Ser	Ile	His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	
			110					115					120			
ccc	tat	gag	cct	gtg	acc	tcg	cgc	ctc	tcg	gac	atc	ttc	agg	ctc	gct	1097
Pro	Tyr	Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	
		125					130					135				
tca	atc	ttc	tca	ggg	aca	ggg	aca	gac	ccg	gcg	gtc	agt	acc	aaa	agc	1145
Ser	Ile	Phe	Ser	Gly	Thr	Gly	Thr	Asp	Pro	Ala	Val	Ser	Thr	Lys	Ser	
	140					145					150					
aac	cac	tgc	ctg	gat	gcc	gcc	aag	gcc	tgc	aac	ctg	aat	gac	aac	tgc	1193
Asn	His	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn	Leu	Asn	Asp	Asn	Cys	
155					160					165					170	
aag	aag	ctt	cgc	tcc	tct	tat	atc	tcc	atc	tgc	aac	cgt	gag	atc	tct	1241
Lys	Lys	Leu	Arg	Ser	Ser	Tyr	Ile	Ser	Ile	Cys	Asn	Arg	Glu	Ile	Ser	
				175					180					185		
ccc	acc	gaa	cgc	tgc	aac	cgc	cgc	aag	tgc	cac	aag	gct	ctg	cgc	cag	1289
Pro	Thr	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His	Lys	Ala	Leu	Arg	Gln	
			190					195					200			
ttc	ttt	gac	cgt	gtg	ccc	agc	gag	tat	acc	tac	cgc	atg	ctc	ttc	tgc	1337
Phe	Phe	Asp	Arg	Val	Pro	Ser	Glu	Tyr	Thr	Tyr	Arg	Met	Leu	Phe	Cys	
		205					210					215				
tcc	tgt	cag	gac	cag	gca	tgt	gct	gag	cgt	cgc	cgg	caa	acc	atc	ctg	1385
Ser	Cys	Gln	Asp	Gln	Ala	Cys	Ala	Glu	Arg	Arg	Arg	Gln	Thr	Ile	Leu	
	220					225					230					
ccc	agt	tgc	tcc	tat	gag	gac	aag	gag	aag	ccc	aac	tgc	ctg	gac	ctg	1433
Pro	Ser	Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	
235					240					245					250	
cgc	agc	ctg	tgt	cgt	aca	gac	cac	ctg	tgc	cgg	tcc	cga	ctg	gca	gat	1481
Arg	Ser	Leu	Cys	Arg	Thr	Asp	His	Leu	Cys	Arg	Ser	Arg	Leu	Ala	Asp	
				255					260					265		
ttc	cac	gcc	aac	tgt	cga	gcc	tcc	tac	cgg	aca	atc	acc	agc	tgt	cct	1529
Phe	His	Ala	Asn	Cys	Arg	Ala	Ser	Tyr	Arg	Thr	Ile	Thr	Ser	Cys	Pro	
			270					275					280			
gcg	gac	aac	tac	cag	gca	tgt	ctg	ggc	tcc	tat	gct	ggc	atg	att	ggg	1577
Ala	Asp	Asn	Tyr	Gln	Ala	Cys	Leu	Gly	Ser	Tyr	Ala	Gly	Met	Ile	Gly	
		285				290						295				
ttt	gat	atg	aca	ccc	aac	tat	gtg	gac	tcc	aac	ccc	acg	ggc	atc	gtg	1625
Phe	Asp	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser	Asn	Pro	Thr	Gly	Ile	Val	
	300					305					310					
gtg	tct	ccc	tgg	tgc	aat	tgt	cgt	ggc	agt	ggg	aac	atg	gaa	gaa	gag	1673
Val	Ser	Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	
315					320					325					330	
tgt	gag	aag	ttc	ctc	agg	gac	ttc	acg	gaa	aac	cca	tgc	ctc	cgg	aat	1721
Cys	Glu	Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	
				335					340					345		

gcc att cag gcc ttt ggt aat ggc aca gat gtg aac atg tct ccc aaa 1769
Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys
350 355 360

ggc ccc tca ctc cca gct acc cag gcc cct cgg gtg gag aag act cct 1817
Gly Pro Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro
365 370 375

tca ctg cca gat gac ctc agt gac agc acc agc ctg ggg acc agt gtc 1865
Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val
380 385 390

atc acc acc tgc aca tct atc cag gag caa ggg ctg aag gcc aac aac 1913
Ile Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn
395 400 405 410

tcc aaa gag tta agc atg tgc ttc aca gag ctc acg aca aac atc agt 1961
Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser
415 420 425

cca ggg agt aaa aag gtg atc aaa ctt aac tca ggc tcc agc aga gcc 2009
Pro Gly Ser Lys Lys Val Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala
430 435 440

aga ctg tcg gct gcc ttg act gcc ctc cca ctc ctg atg ctg acc ttg 2057
Arg Leu Ser Ala Ala Leu Thr Ala Leu Pro Leu Leu Met Leu Thr Leu
445 450 455

gcc ttg taggcctttg gaacccagca caaaagtctt tcaagcaacc cagatatgaa 2113
Ala Leu
460

ctcccgctg acaaaatgga aacacacgca tacacacatg ccacacacag acacacacac 2173

agacacacac acacacacac atacagacgt cgacgcggcc gc 2215

<210> 40
<211> 460
<212> PRT
<213> RAT

<400> 40

Met Leu Val Phe Pro Ser His Tyr Pro Asp Glu Thr Leu Arg Ser Leu
1 5 10 15

Ala Ser Pro Ser Ser Leu Gln Gly Ser Glu Leu His Gly Trp Arg Pro
20 25 30

Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn
35 40 45

Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp
50 55 60

Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val
65 70 75 80

Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys
85 90 95

Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu
100 105 110

Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr
115 120 125

Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr
130 135 140

Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His Cys Leu Asp Ala
145 150 155 160

Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser
165 170 175

Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn
180 185 190

Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro
195 200 205

Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala
210 215 220

Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu
225 230 235 240

Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Ser Leu Cys Arg Thr
245 250 255

Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg
260 265 270

Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala
275 280 285

Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn
290 295 300

Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val Ser Pro Trp Cys Asn
305 310 315 320

Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg
325 330 335

Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly
340 345 350

Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly Pro Ser Leu Pro Ala
355 360 365

Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu
370 375 380

Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser
385 390 395 400

Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met
405 410 415

Cys Phe Thr Glu Leu Thr Thr Asn Ile Ser Pro Gly Ser Lys Lys Val
420 425 430

Ile Lys Leu Asn Ser Gly Ser Ser Arg Ala Arg Leu Ser Ala Ala Leu
435 440 445

Thr Ala Leu Pro Leu Leu Met Leu Thr Leu Ala Leu
450 455 460

<210> 41
<211> 1699
<212> DNA
<213> RAT

<220>
<221> CDS
<222> (67)..(1257)

<400> 41
gcggccgcgt cgaccgacgc ccagcacagg cagagcgctg ccgggtccgc ggcgtccaga 60

cccgcc atg ggg ctc tcc cgg agc ccg cga ccg ccg cta gtg atc 108
Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile
1 5 10

ctg cta ctg gtg ctg tcg ctg tgg cta ccc ctt gga aca gga aac tcc 156
Leu Leu Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser
15 20 25 30

ctt ccc aca gag aac agg ctt gtg aac agc tgt acc cag gcc aga aaa 204
Leu Pro Thr Glu Asn Arg Leu Val Asn Ser Cys Thr Gln Ala Arg Lys
35 40 45

aaa tgc gag gct aat ccc gct tgc aag gct gcc tac cag cac ctg gac 252
Lys Cys Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Asp
50 55 60

tcc tgc acc ccc agt ctc agc agt cca ctg ccc tca ggg gag tct gcc 300
Ser Cys Thr Pro Ser Leu Ser Ser Pro Leu Pro Ser Gly Glu Ser Ala
65 70 75

aca	tct	gca	gcg	tgc	ctt	gaa	gca	gca	cag	caa	ctc	agg	aac	agc	tct	348
Thr	Ser	Ala	Ala	Cys	Leu	Glu	Ala	Ala	Gln	Gln	Leu	Arg	Asn	Ser	Ser	
80						85					90					
ctc	ata	gac	tgc	agg	tgc	cac	cgg	cgc	atg	aag	cac	caa	gct	acc	tgt	396
Leu	Ile	Asp	Cys	Arg	Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	
95					100					105					110	
ctg	gac	att	tat	tgg	acc	gtt	cac	cct	gtc	cga	agc	ctt	ggt	gac	tac	444
Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Pro	Val	Arg	Ser	Leu	Gly	Asp	Tyr	
				115					120					125		
gag	ttg	gac	gtc	tca	ccc	tat	gaa	gac	aca	gtg	acc	agc	aaa	ccc	tgg	492
Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	
			130					135					140			
aaa	atg	aat	ctc	agc	aag	ctg	agc	atg	ctc	aaa	cca	gac	tcc	gac	ctc	540
Lys	Met	Asn	Leu	Ser	Lys	Leu	Ser	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	
		145					150					155				
tgc	ctc	aaa	ttt	gct	atg	ctg	tgt	act	ctt	aac	gac	aag	tgc	gac	cgc	588
Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	
160						165					170					
ctc	cga	aag	gcc	tac	ggg	gag	gcg	tgc	tca	ggg	atc	cgc	tgc	cag	cgc	636
Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Ile	Arg	Cys	Gln	Arg	
175					180					185					190	
cac	ctc	tgc	cta	gct	cag	ctg	cgc	tcc	ttc	ttc	gag	aag	gcg	gca	gag	684
His	Leu	Cys	Leu	Ala	Gln	Leu	Arg	Ser	Phe	Phe	Glu	Lys	Ala	Ala	Glu	
				195					200					205		
tcc	cac	gct	cag	ggc	ctg	ctg	ctg	tgt	ccc	tgt	gca	ccc	gaa	gat	gcg	732
Ser	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Glu	Asp	Ala	
			210					215					220			
ggc	tgt	ggg	gag	cgc	cgg	cgc	aac	acc	atc	gcc	ccc	agt	tgc	gcc	ctc	780
Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Ser	Cys	Ala	Leu	
		225					230					235				
cgg	tct	gtg	gcc	ccc	aac	tgc	cta	gat	ctt	cgg	agc	ttc	tgc	cgt	gcg	828
Pro	Ser	Val	Ala	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Phe	Cys	Arg	Ala	
		240				245					250					
gac	cct	ctg	tgc	aga	tca	cgc	ctg	atg	gac	ttc	cag	acc	cac	tgc	cac	876
Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Met	Asp	Phe	Gln	Thr	His	Cys	His	
255					260					265					270	
cct	atg	gac	atc	ctc	ggg	act	tgt	gca	act	gag	cag	tcc	aga	tgt	ctg	924
Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	
				275					280					285		
cgg	gca	tac	ctg	ggg	cta	att	ggg	act	gcc	atg	acc	cca	aac	ttc	atc	972
Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Ile	
			290				295						300			
agc	aag	gtc	aac	act	act	gtt	gcc	tta	ggc	tgt	acc	tgc	cga	ggc	agt	1020
Ser	Lys	Val	Asn	Thr	Thr	Val	Ala	Leu	Gly	Cys	Thr	Cys	Arg	Gly	Ser	
		305					310					315				
ggc	aac	ctg	cag	gac	gag	tgt	gaa	cag	ctg	gaa	aag	tcc	ttc	tcc	cag	1068
Gly	Asn	Leu	Gln	Asp	Glu	Cys	Glu	Gln	Leu	Glu	Lys	Ser	Phe	Ser	Gln	
		320				325					330					

[illegible]

<210> 42

<211> 397

<212> PRT

<213> RAT

<400> 42

Met Gly Leu Ser Arg Ser Pro Arg Pro Pro Pro Leu Val Ile Leu Leu
1 5 10 15

Leu Val Leu Ser Leu Trp Leu Pro Leu Gly Thr Gly Asn Ser Leu Pro
20 25 30

Thr Glu Asn Arg Leu Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys
35 40 45

Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Asp Ser Cys
50 55 60

Thr Pro Ser Leu Ser Ser Pro Leu Pro Ser Gly Glu Ser Ala Thr Ser
65 70 75 80

Ala Ala Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser Leu Ile
85 90 95

Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp
100 105 110

Ile Tyr Trp Thr Val His Pro Val Arg Ser Leu Gly Asp Tyr Glu Leu
115 120 125

Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met
130 135 140

Asn Leu Ser Lys Leu Ser Met Leu Lys Pro Asp Ser Asp Leu Cys Leu
145 150 155 160

Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg Leu Arg
165 170 175

Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu
180 185 190

Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His
195 200 205

Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys
210 215 220

Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser
225 230 235 240

Val Ala Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro
245 250 255

Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met
260 265 270

Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala
275 280 285

Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys
290 295 300

Val Asn Thr Thr Val Ala Leu Gly Cys Thr Cys Arg Gly Ser Gly Asn
305 310 315 320

Leu Gln Asp Glu Cys Glu Gln Leu Glu Lys Ser Phe Ser Gln Asn Pro
325 330 335

Cys Leu Met Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu
340 345 350

Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Met Gln Gln Gln
355 360 365

Asn Ser Ser Pro Ala Leu Arg Pro Gln Leu Arg Leu Pro Val Leu Ser
370 375 380

Phe Phe Ile Leu Thr Leu Ile Leu Leu Gln Thr Leu Trp
385 390 395

<210> 43
<211> 498
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus GDNFR protein sequence

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (13)..(15)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (17)..(17)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (19)..(19)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (28)..(30)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (37)..(37)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (39)..(40)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (43)..(44)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (48)..(48)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(52)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (54)..(54)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (57)..(58)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (61)..(62)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (70)..(70)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (73)..(75)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (78)..(78)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (83)..(83)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (85)..(90)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (92)..(93)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
<222> (95)..(95)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (97)..(97)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (99)..(100)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (116)..(117)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (120)..(120)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (125)..(125)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (127)..(128)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (130)..(131)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (134)..(135)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (138)..(138)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (144)..(144)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (155)..(156)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (158)..(159)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (161)..(164)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (166)..(170)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (174)..(174)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (187)..(187)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (197)..(198)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (200)..(203)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (205)..(206)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (227)..(228)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (230)..(230)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (239)..(241)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (243)..(243)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (246)..(246)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (254)..(254)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (261)..(262)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (272)..(273)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (278)..(278)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (288)..(288)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (292)..(295)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (297)..(297)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (299)..(299)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (302)..(302)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (304)..(304)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (307)..(308)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (311)..(311)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (314)..(314)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (320)..(320)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (330)..(330)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (332)..(334)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (340)..(340)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (347)..(348)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (356)..(356)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (359)..(360)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (365)..(365)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (375)..(385)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (387)..(387)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (391)..(395)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (397)..(397)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (399)..(399)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (401)..(401)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (404)..(406)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (410)..(413)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (415)..(418)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (420)..(420)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (422)..(422)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (424)..(426)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (428)..(429)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (432)..(432)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (434)..(434)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (437)..(437)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (439)..(439)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (441)..(441)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
<222> (443)..(445)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (448)..(448)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (454)..(457)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (460)..(463)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (465)..(467)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (469)..(470)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (472)..(472)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (475)..(475)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (478)..(479)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (490)..(490)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (494)..(497)
<223> Xaa can be any naturally occurring amino acid

<400> 43

Met	Val	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Pro	Xaa	Pro	Pro	Xaa	Xaa	Xaa	Met
1				5				10						15	

Xaa	Leu	Xaa	Leu	Leu	Ser	Leu	Ala	Leu	Pro	Leu	Xaa	Xaa	Xaa	Leu	Gln
			20					25					30		

Gly Ala Glu Leu Xaa Gly Xaa Xaa Arg Leu Xaa Xaa Asp Cys Val Xaa
35 40 45

Ala Xaa Xaa Xaa Cys Xaa Ala Glu Xaa Xaa Cys Ser Xaa Xaa Tyr Arg
50 55 60

Thr Leu Arg Gln Cys Xaa Ala Gly Xaa Xaa Xaa Asn Thr Xaa Leu Ala
65 70 75 80

Ser Gly Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Ala Xaa Glu
85 90 95

Xaa Leu Xaa Xaa Ser Ser Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met
100 105 110

Lys Lys Glu Xaa Xaa Cys Leu Xaa Ile Tyr Trp Ser Xaa His Xaa Xaa
115 120 125

Leu Xaa Xaa Gly Asn Xaa Xaa Leu Glu Xaa Ser Pro Tyr Glu Pro Xaa
130 135 140

Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Xaa Xaa Ser Xaa Xaa Ser
145 150 155 160

Xaa Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa Lys Ser Asn Xaa Cys Leu
165 170 175

Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Xaa Cys Lys Lys Leu Arg
180 185 190

Ser Ala Tyr Ile Xaa Xaa Cys Xaa Xaa Xaa Xaa Ser Xaa Xaa Glu Arg
195 200 205

Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys
210 215 220

Val Pro Xaa Xaa His Xaa Tyr Gly Met Leu Phe Cys Ser Cys Xaa Xaa
225 230 235 240

Xaa Asp Xaa Ala Cys Xaa Glu Arg Arg Arg Gln Thr Ile Xaa Pro Ser
245 250 255

Cys Ser Tyr Glu Xaa Xaa Glu Lys Pro Asn Cys Leu Asp Leu Arg Xaa
260 265 270

Xaa Cys Arg Thr Asp Xaa Leu Cys Arg Ser Arg Leu Ala Asp Phe Xaa
275 280 285

Thr Asn Cys Xaa Xaa Xaa Xaa Arg Xaa Val Xaa Ser Cys Xaa Ala Xaa
290 295 300

Asn Tyr Xaa Xaa Cys Leu Xaa Ala Tyr Xaa Gly Leu Ile Gly Thr Xaa
305 310 315 320

Met Thr Pro Asn Tyr Val Asp Ser Ser Xaa Thr Xaa Xaa Xaa Val Ala
325 330 335

Pro Trp Cys Xaa Cys Arg Gly Ser Gly Asn Xaa Xaa Glu Glu Cys Glu
340 345 350

Lys Phe Leu Xaa Phe Phe Xaa Xaa Asn Pro Cys Leu Xaa Asn Ala Ile
355 360 365

Gln Ala Phe Gly Asn Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
370 375 380

Xaa Pro Xaa Phe Ser Val Xaa Xaa Xaa Xaa Xaa Thr Xaa Thr Xaa Ala
385 390 395 400

Xaa Arg Val Xaa Xaa Xaa Pro Ser Leu Xaa Xaa Xaa Xaa Ser Xaa Xaa
405 410 415

Xaa Xaa Leu Xaa Thr Xaa Val Xaa Xaa Xaa Cys Xaa Xaa Leu Gln Xaa
420 425 430

Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Glu Xaa Xaa Xaa Cys Phe Xaa
435 440 445

Glu Leu Thr Thr Asn Xaa Xaa Xaa Xaa Ser Gly Xaa Xaa Xaa Xaa Ile
450 455 460

Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Pro Ser Xaa Ala Leu Xaa Xaa Leu
465 470 475 480

Pro Val Leu Met Leu Thr Ala Leu Ala Xaa Leu Leu Ser Xaa Xaa Xaa
485 490 495

Xaa Ser

<210> 44
<211> 489
<212> PRT
<213> Artificial Sequence

<220>
<223> Rat consensus sequence

<220>
<221> misc_feature
<222> (1)..(9)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (11)..(14)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (16)..(16)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (19)..(19)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (22)..(23)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (26)..(26)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (28)..(29)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (31)..(35)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (37)..(39)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (43)..(43)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (45)..(47)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (49)..(49)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (52)..(53)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (56)..(57)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (65)..(65)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (68)..(70)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (72)..(79)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (81)..(82)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (85)..(86)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (88)..(88)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (90)..(90)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (92)..(93)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (109)..(110)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (113)..(113)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (118)..(118)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (120)..(121)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (123)..(124)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (126)..(128)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (131)..(131)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (136)..(136)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (148)..(149)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (151)..(152)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (154)..(157)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (159)..(163)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (167)..(167)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (180)..(180)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (190)..(191)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (193)..(196)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
<222> (198)..(199)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (220)..(221)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (223)..(223)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (232)..(234)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (236)..(236)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (239)..(239)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (247)..(247)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (254)..(255)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (257)..(257)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (266)..(266)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (271)..(271)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (281)..(281)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (285)..(285)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (287)..(288)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (290)..(291)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (293)..(293)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (295)..(295)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (297)..(297)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (300)..(301)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (304)..(304)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (307)..(307)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (313)..(313)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (322)..(323)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (325)..(327)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (333)..(333)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (340)..(341)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (349)..(350)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (352)..(353)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (358)..(358)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (368)..(368)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (371)..(371)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (375)..(376)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (378)..(381)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (383)..(383)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (385)..(390)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (393)..(395)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (397)..(397)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (399)..(402)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (404)..(409)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (411)..(411)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (413)..(415)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (417)..(419)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (421)..(421)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (423)..(423)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (426)..(426)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (428)..(428)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (430)..(434)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (436)..(456)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (458)..(459)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (461)..(462)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (464)..(465)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature

<222> (467)..(468)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (476)..(476)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (478)..(480)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (482)..(484)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (486)..(486)
<223> Xaa can be any naturally occurring amino acid

<400> 44

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Leu Xaa
1 5 10 15

Thr Leu Xaa Ser Leu Xaa Xaa Pro Leu Xaa Leu Xaa Xaa Ser Xaa Xaa
20 25 30

Xaa Xaa Xaa Arg Xaa Xaa Xaa Asp Cys Val Xaa Ala Xaa Xaa Xaa Cys
35 40 45

Xaa Ala Glu Xaa Xaa Cys Ser Xaa Xaa Tyr Arg Thr Leu Arg Gln Cys
50 55 60

Xaa Ala Gly Xaa Xaa Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ala
65 70 75 80

Xaa Xaa Glu Cys Xaa Xaa Ala Xaa Glu Xaa Leu Xaa Xaa Ser Ser Leu
85 90 95

Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Xaa Xaa Cys Leu
100 105 110

Xaa Ile Tyr Trp Ser Xaa His Xaa Xaa Leu Xaa Xaa Gly Xaa Xaa Xaa
115 120 125

Leu Glu Xaa Ser Pro Tyr Glu Xaa Pro Val Thr Ser Arg Leu Ser Asp
130 135 140

Ile Phe Arg Xaa Xaa Ser Xaa Xaa Ser Xaa Xaa Xaa Xaa Asp Xaa Xaa
145 150 155 160

Xaa	Xaa	Xaa	Lys	Ser	Asn	Xaa	Cys	Leu	Asp	Ala	Ala	Lys	Ala	Cys	Asn
				165					170					175	
Leu	Asn	Asp	Xaa	Cys	Lys	Lys	Leu	Arg	Ser	Ala	Tyr	Ile	Xaa	Xaa	Cys
			180					185					190		
Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Glu	Arg	Cys	Asn	Arg	Arg	Lys	Cys	His
			195				200					205			
Lys	Ala	Leu	Arg	Gln	Phe	Phe	Asp	Lys	Val	Pro	Xaa	Xaa	His	Xaa	Tyr
	210					215					220				
Gly	Met	Leu	Phe	Cys	Ser	Cys	Xaa	Xaa	Xaa	Asp	Xaa	Ala	Cys	Xaa	Glu
225					230					235					240
Arg	Arg	Arg	Gln	Thr	Ile	Xaa	Pro	Ser	Cys	Ser	Tyr	Glu	Xaa	Xaa	Glu
				245					250					255	
Xaa	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser	Xaa	Cys	Arg	Thr	Asp	Xaa	Leu
			260					265					270		
Cys	Arg	Ser	Arg	Leu	Ala	Asp	Phe	Xaa	Thr	Asn	Cys	Xaa	Pro	Xaa	Xaa
		275					280					285			
Arg	Xaa	Xaa	Thr	Xaa	Cys	Xaa	Ala	Xaa	Asn	Tyr	Xaa	Xaa	Cys	Leu	Xaa
	290					295					300				
Ala	Tyr	Xaa	Gly	Leu	Ile	Gly	Thr	Xaa	Met	Thr	Pro	Asn	Tyr	Val	Asp
305					310					315					320
Ser	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Val	Ala	Pro	Trp	Cys	Xaa	Cys	Arg	Gly
				325					330					335	
Ser	Gly	Asn	Xaa	Xaa	Glu	Glu	Cys	Glu	Lys	Phe	Leu	Xaa	Xaa	Phe	Xaa
			340					345					350		
Xaa	Asn	Pro	Cys	Leu	Xaa	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Xaa
		355					360					365			
Asp	Val	Xaa	Met	Ser	Gln	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Ala
	370					375					380				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Val	Xaa	Xaa	Xaa	Pro	Xaa	Leu	Xaa	Xaa
385					390					395					400
Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Xaa	Val	Xaa	Xaa	Xaa	Cys
				405					410					415	

Xaa Xaa Xaa Gln Xaa Gln Xaa Leu Lys Xaa Asn Xaa Ser Xaa Xaa Xaa
420 425 430

Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
435 440 445

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Xaa Xaa Ala Xaa Xaa Ser Xaa
450 455 460

Xaa Leu Xaa Xaa Leu Pro Val Leu Met Leu Thr Xaa Leu Xaa Xaa Xaa
465 470 475 480

Leu Xaa Xaa Xaa Leu Xaa Glu Thr Ser
485

<210> 45
<211> 3209
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1091)..(1091)
<223> N in position 1091 indicates any nucleic acid.

<220>
<221> misc_feature
<222> (2078)..(2078)
<223> N in position 2078 indicates a position of divergence between
different receptor clones.

<220>
<221> misc_feature
<222> (2256)..(2294)
<223> N in positions 2256 to 2294 indicates positions of divergence
between different receptor clones.

<400> 45
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgctctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tatttttttt ttcttttttt tcttttccta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240
taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt 300
cggacctgaa ccctaaaag cggaaccgcc tcccgccctc gccatcccgg agctgagtcg 360
ccggcggcgg tggctgctgc cagaccggga gtttcctctt tctactggatg gagctgaact 420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa 480
gaccagcgg cggtcggga tttttttggg ggggcgggga ccagcccgc gccggcacca 540
tgttcctggc gacctgtac ttcgcgctgc cgctcttga cttgctcctg tcggccgaag 600

tgagcggcgg	agaccgcctg	gattgcgtga	aagccagtga	tcagtgcctg	aaggagcaga	660
gctgcagcac	caagtaccgc	acgctaaggc	agtgcgtggc	gggcaaggag	accaaacttca	720
gcctggcatc	cggcctggag	gccaaaggatg	agtgccgcag	cgccatggag	gccctgaagc	780
agaagtcgct	ctacaactgc	cgctgcaagc	ggggatatgaa	gaaggagaag	aactgcctgc	840
gcatttactg	gagcatgtac	cagagcctgc	agggaaatga	tctgctggag	gattcccat	900
atgaaccagt	taacagcaga	ttgtcagata	tattccgggt	ggccccattc	atatcagatg	960
tttttcagca	agtggagcac	attcccaaag	ggaacaactg	cctggatgca	gcgaaggcct	1020
gcaacctcga	cgacatttgc	aagaagtaca	ggtcggcgta	catcaccccg	tgcaccacca	1080
gcgtgtccaa	ngatgtctgc	aaccgccgca	agtgccacaa	ggccctccgg	cagttctttg	1140
acaaggcccc	ggccaagcac	agctacggaa	tgctcttctg	ctcctgccgg	gacatgcct	1200
gcacagagcg	gagggcagag	accatcgtgc	ctgtgtgctc	ctatgaagag	agggagaagc	1260
ccaactgttt	gaatttgcag	gactcctgca	agacgaatta	catctgcaga	tctcgccttg	1320
cggatttttt	taccaactgc	cagccagagt	caaggctctgt	cagcagctgt	ctaaaggaaa	1380
actacgtga	ctgcctcctc	gcctactcgg	ggcttattgg	cacagtcatg	acccccaaact	1440
acatagactc	cagtagcctc	agtgtggccc	catggtgtga	ctgcagcaac	agtgggaacg	1500
acctagaaga	gtgcttgaaa	tttttgaatt	tcttcaagga	caatacatgt	cttaaaaatg	1560
caattcaagc	ctttggcaat	ggctccgatg	tgaccgtgtg	gcagccagcc	ttcccagtac	1620
agaccaccac	tgccactacc	accactgccc	tccgggttaa	gaacaagccc	ctggggccag	1680
cagggtctga	gaatgaaatt	cccactcatg	ttttgccacc	gtgtgcaa	ttacaggcac	1740
agaagctgaa	atccaatgtg	tcgggcaata	cacacctctg	tatttccaat	ggtaattatg	1800
aaaaagaagg	tctcgggtgct	tccagccaca	taaccacaaa	atcaatggct	gtcctccaa	1860
gctgtggtct	gagcccactg	ctggctcctgg	tggttaaccgc	tctgtccacc	ctattatctt	1920
taacagaaac	atcatagctg	cattaaaaaa	atacaatatg	gacatgtaa	aagacaaaaa	1980
ccaagtatc	tgtttcctgt	tctcttgtat	agctgaaatt	ccagtttagg	agctcagttg	2040
agaaacagtt	ccattcaact	ggaacatttt	tttttttncc	ttttaagaaa	gcttcttgtg	2100
atccttcggg	gcttctgtga	aaaacctgat	gcagtgtctc	atccaaactc	agaaggcttt	2160
gggatatgct	gtatttttaa	gggacagttt	gtaacttggg	ctgtaaagca	aactggggct	2220
gtgttttcga	tgatgatgat	catcatgatc	atgatnnnnn	nnnnnnnnnn	nnnnnnnnnn	2280
nnnnnnnnnn	nnngatttt	aacagtttta	cttctggcct	ttcctagcta	gagaaggagt	2340
taatatttct	aaggtaactc	ccatatctcc	tttaatgaca	ttgatttcta	atgatataaa	2400
tttcagccta	cattgatgcc	aagctttttt	gccacaaaga	agattcttac	caagagtggg	2460
ctttgtggaa	acagctggta	ctgatgttca	cctttatata	tgtactagca	ttttccacgc	2520

tgatgtttat gtactgtaaa cagttctgca ctcttgtaaa aaagaaaaaa cacctgtcac 2580
atccaaatat agtatctgtc ttttcgtcaa aatagagagt ggggaatgag tgtgccgatt 2640
caatacctca atccctgaac gacactctcc taatcctaag ccttacctga gtgagaagcc 2700
ctttacctaa caaaagtcca atatagctga aatgtcgtc taatactctt tacacatatg 2760
aggttatatg tagaaaaaaa ttttactact aaatgatttc aactattggc tttctatatt 2820
ttgaaagtaa tgatattgtc tcattttttt actgatgggt taatacaaaa tacacagagc 2880
ttgtttcccc tcataagtag tgttcgtctc gatatgaact tcacaaatac agctcatcaa 2940
aagcagactc tgagaagcct cgtgctgtag cagaaagtcc tgcacatcat gactgtggac 3000
aggcaggagg aacagaaca gacaagcatt gtcttttgtc attgctcgaa gtgcaagcgt 3060
gcatacctgt ggagggaact ggtggctgct tgtaaagtgt ctgcagcatc tcttgacaca 3120
cttgtcatga cacaatccag taccttggtt ttcaggttat ctgacaaagg cagctttgat 3180
tgggacatgg aggcattggc aggccggaa 3209

<210> 46
<211> 508
<212> DNA
<213> HUMAN

<400> 46
tctggcctcg gaacacgcca ttctccgccc cgcttccaat aaccactaac atccctaacg 60
agcatccgag ccgagggtc tgctcggaaa tcgtcctggc ccaactcggc ccttcgagct 120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag 180
tgagcccgga aaggggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta 240
aataaacaaa ctggctcctc gccgcagctg gacgcggctc gttgagtcca ggttgggtcg 300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccgag ctgagtcgcc 360
ggcggcggtg gctgctgcca gaccggagt ttctctttt actggatgga gctgaacttt 420
gggcggccag agcagcacag ctgtccgggg atcgtgcac gctgagctcc ctcggaaga 480
cccagcggcg gctcgggatt tttttggg 508

<210> 47
<211> 510
<212> DNA
<213> HUMAN

<400> 47
aatctggcct cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga ttaccgcac tttttttttt ttctttttt tcttttccta gcgcagataa 180
agtgagcccg gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240

taaataaaca aactggctcc tcgccgcagc tggacgcggt cggttgagtc caggttgggt	300
cggacctgaa cccctaaaag cggaaccgcc tcccgccctc gccatcccgg agctgagtcg	360
ccggcggcgg tggtctgctgc cagaccgcga gtttcctctt tcaactggatg gagctgaact	420
ttgggcggcc agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcggcaa	480
gaccagcgg cggtctggga tttttttggg	510

<210> 48
 <211> 1927
 <212> DNA
 <213> HUMAN

<220>
 <221> misc_feature
 <222> (550)..(550)
 <223> N in position 550 indicates any nucleic acid

<400> 48	
tctggcctcg gaacacgcca ttctccgcgc cgcttccaat aaccactaac atccctaacg	60
agcatccgag ccgagggctc tgctcggaaa tcgtcctggc ccaactcggc ccttcgagct	120
ctcgaagatt accgcatcta tttttttttt cttttttttt ttttcctagc gcagataaag	180
tgagcccgga aagggaagga gggggcgggg acaccattgc cctgaaagaa taaataagta	240
aataaaciaa ctggctcctc gccgcagctg gacgcggtcg gttgagtcca ggttgggtcg	300
gacctgaacc cctaaaagcg gaaccgcctc ccgccctcgc catcccggag ctgagtcgcc	360
ggcggcgggtg gctgctgcca gaccgggagt ttctcttttc actggatgga gctgaacttt	420
gggcggccag agcagcacag ctgtccgggg atcgctgcac gctgagctcc ctcggaaga	480
cccagcggcg gctcgggatt tttttggggg ggcggggacc agccccgcgc cggcaccatg	540
ttcttgccgn ccctgtactt cgcgctgccg ctcttggaact tgctcctgtc ggccgaagtg	600
agcggcggag accgcctgga ttgcgtgaaa gccagtgatc agtgccctgaa ggagcagagc	660
tgcagacca agtaccgcac gctaaggcag tgcgtggcgg gcaaggagac caacttcagc	720
ctggcatccg gcctggaggc caaggatgag tgccgcagcg ccatggaggc cctgaagcag	780
aagtcgctct acaactgccg ctgcaagcgg ggtatgaaga aggagaagaa ctgcctgcgc	840
atttactgga gcatgtacca gagcctgcag ggaaatgatc tgctggagga tccccatat	900
gaaccagtta acagcagatt gtcagatata ttccgggttg tccattcat atcagatgtt	960
tttcagcaag tggagcacat tcccaaaggg aacaactgcc tggatgcagc gaaggcctgc	1020
aacctcgacg acatttgcaa gaagtacagg tcggcgtaca tcaccccgctg caccaccagc	1080
gtgtccaacg atgtctgcaa ccgccgcaag tgccacaagg ccctccggca gttctttgac	1140
aagggtcccgg ccaagcacag ctacggaatg ctcttctgct cctgccggga catgcctgc	1200

acagagcgga	ggcgacagac	catcgtgcct	gtgtgctcct	atgaagagag	ggagaagccc	1260
aactgtttga	atttgcagga	ctcctgcaag	acgaattaca	tctgcagatc	tcgccttgcg	1320
gattttttta	ccaactgcc	gccagagtca	aggtctgtca	gcagctgtct	aaaggaaaac	1380
tacgctgact	gcctcctcgc	ctactcgggg	cttattggca	cagtcatgac	ccccaactac	1440
atagactcca	gtagcctcag	tgtggcccca	tgggtgtgact	gcagcaacag	tgggaacgac	1500
ctagaagagt	gcttgaaatt	tttgaatttc	ttcaaggaca	atacatgtct	taaaaatgca	1560
attcaagcct	ttggcaatgg	ctccgatgtg	accgtgtggc	agccagcctt	cccagtacag	1620
accaccactg	ccactaccac	cactgccctc	cgggttaaga	acaagcccct	ggggccagca	1680
gggtctgaga	atgaaattcc	cactcatgtt	ttgccaccgt	gtgcaaattt	acaggcacag	1740
aagctgaaat	ccaatgtgtc	gggcaataca	cacctctgta	tttccaatgg	taattatgaa	1800
aaagaaggtc	tcggtgcttc	cagccacata	accacaaaat	caatggctgc	tcctccaagc	1860
tgtggtctga	gccactgct	ggtcctggtg	gtaaccgctc	tgtccaccct	attatcttta	1920
acagaaa						1927

<210> 49
<211> 1929
<212> DNA
<213> HUMAN

<400> 49	
aatctggcct	cggaacacgc cattctccgc gccgcttcca ataaccacta acatccctaa 60
cgagcatccg	agccgagggc tctgctcgga aatcgtcctg gcccaactcg gcccttcgag 120
ctctcgaaga	ttaccgcac tatttttttt ttcttttttt tcttttccta gcgcagataa 180
agtgcgccc	gaaaggggaag gagggggcgg ggacaccatt gccctgaaag aataaataag 240
taaataaaca	aactggctcc tcgcgcagc tggacgcggt cggttgagtc cagggtgggt 300
cggacctgaa	cccctaaaag cggaaccgcc tcccgcctc gccatcccgg agctgagtcg 360
ccggcggcgg	tggctgctgc cagaccgga gtttctctt tctactggatg gagctgaact 420
ttgggcggcc	agagcagcac agctgtccgg ggatcgctgc acgctgagct ccctcgga 480
gaccagcgg	cggctcggga tttttttggg ggggcgggga ccagccccgc gccggcacca 540
tgttctctgg	gacctgtac ttgcgcgtgc cgctcttggc cttgctcctg tcggccgaag 600
tgagcggcgg	agaccgcctg gattgcgtga aagccagtga tcagtgcctg aaggagcaga 660
gctgcagcac	caagtaccgc acgctaaggc agtgcgtggc gggcaaggag accaacttca 720
gcctggcatc	cggcctggag gcccaaggatg agtgccgcag cgccatggag gccctgaagc 780
agaagtcgct	ctacaactgc cgctgcaagc ggggtatgaa gaaggagaag aactgcctgc 840
gcatttactg	gagcatgtac cagagcctgc agggaaatga tctgctggag gattccccat 900
atgaaccagt	taacagcaga ttgtcagata tattccgggt ggtcccatc atatcagatg 960

tttttcagca agtgggagcac attcccaaag ggaacaactg cctggatgca gcgaaggcct 1020
gcaacctcga cgacatttgc aagaagtaca ggtcggcgta catcaccccg tgcaccacca 1080
gcgtgtccaa cgatgtctgc aaccgccgca agtgccacaa ggccctccgg cagttctttg 1140
acaaggtccc ggccaagcac agctacggaa tgctcttctg ctctgcccgg gacatcgctt 1200
gcacagagcg gaggcgacag accatcgtgc ctgtgtgctc ctatgaagag agggagaagc 1260
ccaactgttt gaatttgcag gactcctgca agacgaatta catctgcaga tctcgcttg 1320
cggatttttt taccaactgc cagccagagt caagggtctgt cagcagctgt ctaaaggaaa 1380
actacgctga ctgcctctc gcctactcgg ggcttattgg cacagtcatg acccccaact 1440
acatagactc cagtagcctc agtgtggccc catggtgtga ctgcagcaac agtgggaacg 1500
acctagaaga gtgcttgaaa tttttgaatt tcttcaagga caatacatgt cttaaaaatg 1560
caattcaagc ctttggcaat ggctccgatg tgaccgtgtg gcagccagcc tcccagtac 1620
agaccaccac tgccactacc accactgccc tccgggttaa gaacaagccc ctggggccag 1680
caggggtctga gaatgaaatt cccactcatg ttttgccacc gtgtgcaaatt ttacaggcac 1740
agaagctgaa atccaatgtg tcgggcaata cacacctctg tatttccaat ggtaattatg 1800
aaaaagaagg tctcgggtgt tccagccaca taaccacaaa atcaatggct gctcctccaa 1860
gctgtggtct gagcccactg ctggctctgg tggtaacgc tctgtccacc ctattatctt 1920
taacagaaa 1929

<210> 50
<211> 699
<212> DNA
<213> HUMAN

<400> 50
gtcggcgctac atcaccccg gcaccaccag cgtgtccaat gatgtctgca accgccgcaa 60
gtgccacaag gccctccggc agttctttga caagggtccc gccaagcaca gctacggaat 120
gctcttctgc tcctgccggg acatcgctg cacagagcgg aggcgacaga ccatcgtgcc 180
tgtgtgctcc tatgaagaga gggagaagcc caactgtttg aatttgcagg actcctgcaa 240
gacgaattac atctgcagat ctgccttgc ggattttttt accaactgcc agccagagtc 300
aagggtctgtc agcagctgtc taaaggaaaa ctacgctgac tgcctcctcg cctactcggg 360
gcttattggc acagtcatga ccccaacta catagactcc agtagcctca gtgtggcccc 420
atgggtgtgac tgcagcaaca gtgggaacga cctagaagag tgcttgaaat ttttgaattt 480
cttcaaggac aatacatgtc ttaaaaatgc aattcaagcc tttggcaatg gctccgatgt 540
gaccgtgtgg cagccagcct tcccagtaca gaccaccact gccgtacca ccactgcctt 600
ccgggttaag aacaagcccc tggggccagc aggggtctgag aatgaaattc ccactcatgt 660

tttgccaccg tgtgcaaatt tacaggcaca gaagctgaa

699

<210> 51
<211> 2158
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1027)..(1027)
<223> N in position 1027 indicates a position of divergence between
different receptor clones.

<220>
<221> misc_feature
<222> (1205)..(1243)
<223> N in positions 1205 to 1243 indicates positions of divergence
between different receptor clones.

<400> 51
gtcggcgtag atcaccctgt gcaccaccag cgtgtccaat gatgtctgca accgccgcaa 60
gtgccacaag gccctccggc agttctttga caaggtcccg gccaagcaca gctacggaat 120
gctcttctgc tcctgccggg acatcgcttg cacagagcgg aggcgacaga ccatcgtgcc 180
tgtgtgtctc tatgaagaga gggagaagcc caactgtttg aatttgcagg actcctgcaa 240
gacgaattac atctgcagat ctgccttg gcgatttttt accaactgcc agccagagtc 300
aaggtctgtc agcagctgtc taaaggaaaa ctacgtgtac tgctctctcg cctactcggg 360
gcttattggc acagtcatga cccccaacta catagactcc agtagcctca gtgtggcccc 420
atggtgtgac tgcagcaaca gtgggaacga cctagaagag tgcttgaaat ttttgaattt 480
cttcaaggac aatacatgtc ttaaaaatgc aattcaagcc tttggcaatg gctccgatgt 540
gaccgtgtgg cagccagcct tcccagtaca gaccaccact gccgctacca ccaactgcct 600
ccgggttaag aacaagcccc tggggccagc aggggtctgag aatgaaattc ccaactcatgt 660
tttgccaccg tgtgcaaatt tacaggcaca gaagctgaaa tccaatgtgt cgggcaatac 720
acacctctgt atttccaatg gtaattatga aaaagaaggt ctcggtgctt ccagccacat 780
aaccacaaaa tcaatggctg ctctctcaag ctgtgggtctg agcccactgc tggctcctggt 840
ggtaaccgct ctgtccacc tattatcttt aacagaaaca tcatagctgc attaaaaaaa 900
tacaatatgg acatgtaaaa agacaaaaac caagttatct gtttctgtt ctcttgata 960
gctgaaattc cagtttagga gctcagttga gaaacagttc cattcaactg gaacattttt 1020
ttttttncct ttaagaaag cttctgtgta tccttcgggg cttctgtgaa aaacctgatg 1080
cagtgtcca tccaaactca gaaggctttg ggatatgctg tatttttaaag ggacagtttg 1140
taacttgggc tgtaaagcaa actggggctg tgttttcgat gatgatgatc atcatgatca 1200
tgatnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnngatttta acagttttac 1260

ttctggcctt tcctagctag agaaggagtt aatatttcta aggtaactcc catatctcct 1320
ttaatgacat tgattttctaa tgatataaat ttcagcctac attgatgcc a gctttttttg 1380
ccacaaagaa gattcttacc aagagtgggc tttgtggaaa cagctggtac tgatgttcac 1440
ctttatatat gtactagcat tttccacgct gatgtttatg tactgtaaac agttctgcac 1500
tcttgtacaa aagaaaaaac acctgtcaca tccaaatata gtatctgtct tttcgtcaaa 1560
atagagagtg gggaatgagt gtgccgattc aatacctcaa tccctgaacg acactctcct 1620
aatcctaagc cttacctgag tgagaagccc tttacctaac aaaagtccaa tatagctgaa 1680
atgtcgctct aatactcttt acacatatga ggttatatgt agaaaaaaat tttactacta 1740
aatgatttca actattggct ttctatatatt tgaaagtaat gatattgtct cattttttta 1800
ctgatggttt aatacaaaaat acacagagct tgtttccctc cataagtagt gttecgctctg 1860
atatgaactt cacaaataca gctcatcaaa agcagactct gagaagcctc gtgctgtagc 1920
agaaagtctt gcatcatgtg actgtggaca ggcaggagga aacagaacag acaagcattg 1980
tcttttgtca ttgctcgaag tgcaagcgtg catacctgtg gagggaaactg gtggctgctt 2040
gtaaagtctt tgcagcatct cttgacacac ttgtcatgac acaatccagt accttggttt 2100
tcaggttatc tgacaaaggc agctttgatt gggacatgga ggcattgggca ggccggaa 2158

<210> 52
<211> 659
<212> DNA
<213> HUMAN

<400> 52
gaatttgcag gactcctgca agacgaatta catctgcaga tctcgccttg cggattttttt 60
taccaactgc cagccagagt caaggtctgt cagcagctgt ctaaaggaaa actacgctga 120
ctgcctcctc gcctactcgg ggcttatttg cacagtcatg accccaact acatagactc 180
cagtagcctc agtgtggccc catggtgtga ctgcagcaac agtgggaacg acctagaaga 240
gtgcttgaaa tttttgaatt tcttcaagga caatacatgt cttaaaaatg caattcaagc 300
ctttggcaat ggctccgatg tgaccgtgtg gcagccagcc ttcccagta c agaccaccac 360
tgccactacc accactgccc tccgggttaa gaacaagccc ctggggccag cagggctctga 420
gaatgaaatt cccactcatg ttttgccacc gtgtgcaa at ttacaggcac agaagctgaa 480
atccaatgtg tcgggcaata cacacctctg tatttccaat ggtaattatg aaaaagaagg 540
tctcgggtgct tccagccaca taaccacaaa atcaatggct gctcctccaa gctgtggtct 600
gagcccactg ctggctcctg tggttaaccgc tctgtccacc ctattatctt taacagaaa 659

<210> 53
<211> 630
<212> DNA
<213> HUMAN

<400> 53
acatctgcag atctcgcctt gcggattttt ttaccaactg ccagccagag tcaaggctctg 60
tcagcagctg tctaaaggaa aactacgctg actgcctcct cgcctactcg gggcttattg 120
gcacagtcac gacccccaac tacatagact ccagtagcct cagtgtggcc ccatgggtgtg 180
actgcagcaa cagtgggaac gacctagaag agtgcttgaa atttttgaat ttcttcaagg 240
acaatacatg tcttaaaaaat gcaattcaag cttttggcaa tggctccgat gtgaccgtgt 300
ggcagccagc cttcccagta cagaccacca ctgccactac caccactgcc ctccgggtta 360
agaacaagcc cctgggggcca gcagggtctg agaatgaaat tccactcat gttttgccac 420
cgtgtgcaaa ttacaggca cagaagctga aatccaatgt gtcgggcaat acacacctct 480
gtatttccaa tggttaattat gaaaaagaag gtctcgggtgc ttccagccac ataaccacaa 540
aatcaatggc tgctcctcca agctgtggtc tgagcccact gctggctctg gtggttaaccg 600
ctctgtccac cctattatct ttaacagaaa 630

<210> 54
<211> 1076
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (586)..(586)
<223> N in position 586 indicates a position of divergence between
different receptor clones.

<220>
<221> misc_feature
<222> (764)..(802)
<223> N in positions 764 to 802 indicates positions of divergence
between different receptor clones.

<400> 54
tgggaacgac ctagaagagt gcttgaaatt tttgaatttc ttcaaggaca atacatgtct 60
taaaaatgca attcaagcct ttggcaatgg ctccgatgtg accgtgtggc agccagcctt 120
cccagtacag accaccactg ccactaccac cactgccctc cgggttaaga acaagcccct 180
ggggccagca gggctctgaga atgaaattcc cactcatgtt ttgccaccgt gtgcaaattt 240
acaggcacag aagctgaaat ccaatgtgtc gggcaatata cacctctgta tttccaatgg 300
taattatgaa aaagaaggct tcgggtgcttc cagccacata accacaaaat caatggctgc 360
tcctccaagc tgtggtctga gccactgct ggtcctgggtg gtaaccgctc tgtccaccct 420
attatcttta acagaaacat catagctgca ttaaaaaaat acaatatgga catgtaaaaa 480
gacaaaaacc aagttatctg tttcctgttc tcttgatatag ctgaaattcc agtttaggag 540
ctcagttgag aaacagttcc attcaactgg aacatTTTTT tttttncctt ttaagaaagc 600

ttcttgtgat ccttcggggc ttctgtgaaa aacctgatgc agtgctccat ccaaactcag 660
aaggcttttg gatatgctgt attttaaagg gacagtttgt aacttgggct gtaaagcaaa 720
ctggggctgt gttttcgaat atgatgatca tcatgatcat gatnnnnnnn nnnnnnnnnn 780
nnnnnnnnnn nnnnnnnnnn nngattttta cagttttact tctggccttt cctagctaga 840
gaaggagtta atattttctaa ggtaactccc atatctcctt taatgacatt gattttctaatt 900
gatataaatt tcagcctaca ttgatgccaa gcttttttgc cacaagaag attcttacca 960
agagtgggct ttgtggaaac agctggtact gatgttcacc tttatatatg tactagcatt 1020
ttccacgctg atgtttatgt actgtaaaca gttctgcact cttgtacaaa agaaaa 1076

<210> 55
<211> 1059
<212> DNA
<213> HUMAN

<400> 55
agtgttgaa atttttgaat ttcttcaagg acaatacatg tcttaaaaat gcaattcaag 60
cctttggcaa tggctccgat gtgaccgtgt ggcagccagc cttcccagta cagaccacca 120
ctgccactac caccactgcc ctccgggtta agaacaagcc cctggggcca gcagggtctg 180
agaatgaaat tcccactcat gttttgccac cgtgtgcaaa tttacaggca cagaagctga 240
aatccaatgt gtcgggcaat acacacctct gtattttcaa tggtaattat gaaaaagaag 300
gtctcgggtgc ttccagccac ataaccacaa aatcaatggc tgctcctcca agctgtggtc 360
tgagcccact gctggctctg gtggttaaccg ctctgtccac cctattatct ttaacagaaa 420
catcatagct gcattaaaaa aatacaatat ggacatgtaa aaagacaaaa accaagttat 480
ctgtttcctg ttctcttgta tagctgaaat tccagtttag gagctcagtt gagaaacagt 540
tccattcaac tggaacattt tttttttttt cttttaagaa agcttcttgt gatccttttg 600
ggcttctgtg aaaaacctga tgcagtgtct catccaaact cagaaggctt tgggatatgc 660
tgtattttta agggacagtt tgtaacttgg gctgtaaagc aaactggggc tgtgttttcg 720
atgatgatga tgatcatgat gatgatcatc atgatcatga tgatgatcat catgatcatg 780
atgatgattt taacagtttt acttctggcc tttcctagct agagaaggag ttaatatattc 840
taaggtaact cccatatctc ctttaatgac attgatttct aatgatataa atttcagcct 900
acattgatgc caagcttttt tgccacaaag aagattctta ccaagagtgg gctttgtgga 960
aacagctgggt actgatgttc acctttatat atgtactagc attttccacg ctgatgttta 1020
tgtactgtaa acagttctgc actcttgtac aaaagaaaa 1059

<210> 56
<211> 468
<212> PRT
<213> Mus musculus

<400> 56

Met Phe Leu Ala Thr Leu Tyr Phe Val Leu Pro Leu Leu Asp Leu Leu
1 5 10 15

Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
20 25 30

Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
35 40 45

Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
50 55 60

Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80

Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95

Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110

Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125

Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
130 135 140

Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
145 150 155 160

Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
165 170 175

Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
180 185 190

His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
195 200 205

Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Val Ala Cys Thr Glu Arg
210 215 220

Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
225 230 235 240

Pro Asn Cys Leu Asn Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
245 250 255

Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
260 265 270

Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
275 280 285

Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser
290 295 300

Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn
305 310 315 320

Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr
325 330 335

Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr
340 345 350

Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Thr Ala Thr Thr Thr
355 360 365

Thr Ala Phe Arg Ile Lys Asn Lys Pro Ser Gly Pro Ala Cys Ser Glu
370 375 380

Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala
385 390 395 400

Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser
405 410 415

Asp Asn Asp Tyr Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile
420 425 430

Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Gly Leu Ser Ser Leu
435 440 445

Pro Val Met Val Phe Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu
450 455 460

Ala Glu Thr Ser
465

<210> 57
<211> 12
<212> PRT
<213> Unknown

<220>
<223> Synthetic peptide sequence of arrestin

<400> 57

Val Phe Glu Glu Phe Ala Arg Gln Asn Leu Lys Cys
1 5 10

<210> 58
<211> 8
<212> PRT
<213> Unknown

<220>
<223> FLAG peptide sequence

<400> 58

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 59
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 59
ctgcaagaag ctgcgctcc

19

<210> 60
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer sequence

<400> 60
cttgctcctca taggagcagc

20

<210> 61
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Flag protein sequence

<400> 61

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5